$F_2$ 2202-2209/Region: nucleotide-binding motif A (P-loop)  $F_2$ 2530-2537/Region: nucleotide-binding motif A (P-loop)

ò

RESULT 10

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C;Species: Halobacterrium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84325
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
J. Letthauser, B.; Kehler, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable, Jung, K.H.; Alam, M.; Freitas, T.
Jung, K.H.; Alam, M.; Freitas, T.
Anthors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
A;Title: Genome sequence of Halobacterium species NRC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig. 22 [imported] - Arabidopsis thaliana (cipes)
Cipecies: Arabidopsis thaliana (mouse-ear cress)
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R;Theologis, A.; Ecker, U.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Jin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 10-11.00712
A;Reference number: A66141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-501 <MCD>
A;Cross-references: EMBL:AL109731; PIDN:CAB52037.1; GSPDB:GN00067; SPDB:SPBC19C2.10
A;Experimental source: strain 972h-; cosmid c19C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T39801
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M. submitted to the EMBL Data Library, July 1999
A;Reference number: Z21880
A;Accession: T39801
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
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hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1
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llarity 41.7%; Pred. No. 56;
Conservative 3; Mismatches 4; Indels
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Pred. No. 48;
1; Mismatches
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
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A;Introns: 196/3
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C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C.Accession: 70655
B.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Maturhors: Sqares, M.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Maturhors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MuID:98295987; PMID:9634230
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A,Residues: 1-274 <LAM>
A,Suber authors at a polisipoprotein B
C,Superfamily: apolispoprotein B
C,Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
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A;Readues: 1-499 <COL>
A;Cross-references: GB:283864; GB:Al123456; NID:g3261687; PIDN:CAB06212.1; PID:e301250; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Accession: Bbuysu
R.Law, A.; Soctt, J.
J. Lipid Res. 31, 1109-1120, 1990
A.Title: A cross-species comparison of the apolipoprotein B domain that binds to the I
A;Reference number: A60950; NUID:90324804; PMID:2373961
A;Accession: B60950
A;Accession: tyme: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        apolipoprotein B-100 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
C;Accession: B60950
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                                                                                                            Query Match 56.7%; Score 38; DB 2; Length 4568; Best Local Similarity 41.7%; Pred. No. 2.7e+02; Matches 5; Conservative 3; Mismatches 4; Indels
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Best Local Similarity Matches 6; Conser 4 WXRNMRKVR 12 39 WDRNLRKFR 47

ઠ 셤 RESULT 11

Query Match

55.2%; Score 37; DB 2; 54.5%; Pred. No. 47; iive 2; Mismatches 3

Conservative

Best Local Similarity Matches 6; Conser

A; Gene: Rv3854c Query Match

Genetics:

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hypothetical sh3-containing protein C, Species: Schizosaccharomyces pombe

RESULT 12 T39801

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.,Status: preliminary
.,Molecule type: DDR.
.,Residues: 1-124 <STO>
.,Cross-references: GB:AE005173; NID:g4587555; PIDN:AAD25786.1; GSPDB:GN00141
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0
                                                                                                                                                            53.7%; Score 36; DB 2; Length 124; 50.0%; Pred. No. 19; ive 3; Mismatches 2; Indels
                                                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                ;,Genetics:
,Gene: F1511.22
,Map position: 1
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2 FOWXRNMRKV 11 |:| |: ||: 11 FRWSRSRRKI 20

Pothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)

'Species: Nostoc sp.
'Note: Nostoc sp.
'Accession: AD2346
'Accession: AD2346
'Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
'Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana; Reference number: AD3346
'Accession: AD3346
'Status: preliminary
'Residues: 1-298 KAUR.
'Cross-references: GB:BA000019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179
'Experimental source: strain PCC 7120
'Genetics:
'Genetics:

Gaps . 0 Query Match 53.7%; Score 36; DB 2; Length 298; Best Local Similarity 66.7%; Pred. No. 45; Matches 6; Conservative 0; Mismatches 3; Indels

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earch completed: February 21, 2003, 08:02:44 ob time: 11.6047 secs

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SEQUENCE FROM N.A.
TISSUE=Mammary gland;
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TISSUE=Prostate;
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                                                                                                 February 21, 2003, 07:28:06; Search time 5.2093 Seconds (without alignments) 95.544 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                       otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                          112892 segs, 41476328 residues
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TRFL_CAPH
NLA_DROME
TRFL_HORSE
TRFL_MOUSE
TRFL_MOUSE
TRFL_HORSE
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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67
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Cho \mathbf{x}.\mathbf{x} , \mathbf{x} , Genetic Engineering Research Institute / Taejon, Korea. Thesis (1994),
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferroxin A;
Lattoferroxin B; Lactoferroxin C].
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

TISSUE=Mmmmary gland;

MEDLINE=20384839; PubMed=2402455;

Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;

"Complete nucleotide sequence of human mammary gland lactoferrin.";

Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                          Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
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Liang Q., Jimenz=Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
submitted (DEC-1991) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE-Bone marrow; Wel X., Han J., Rado T.A.; "Human neutrophil lactoferrin coding and 5' flanking region DNA "Human neutrophil lactoferrin coding and 5' flanking region DNA
                                                                             TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16786; Q16789; Q00756; Q9H1Z3; Q96KZ4;
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TISSUE=Mammary gland;
Cheng H., Chen X., Huan L.;
"CDNA cloning and sequence analysis of human lactoferrin.";
submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
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SEQUENCE OF 237-711 FROM N.A.
MCCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.,
Submitted (MAR-1997) to the EMBL/Genbank/DDBJ databases. EXEMY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
"Mol. Biol. 209:711-734(1989). "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of M. and C-terminal domains."; M. and C-terminal domains."; Blochim. Biophys. Acta 670:243-254 (1981). SEQUENCE OF 609-711. MEDLINE-82262043; PubMed=7049727; Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J., MEDLINE=82046817; PubMed=6794640; Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J., MEDLINE=97156796; PubMed=9003186; Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W., Baker E.N.; "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-SEGUENCE OF 436-711 FROM N.A.
MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz B.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library an expression of mRNA during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987). MEDLINE=55076667; PubMed=6510420;
MEDLINE=55076667; PubMed=6510420;
MELZ-Bourigue M.-H., JOLISE J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
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comparisons with other transferrins.";
Eur. J. Biochem. 145:659-666(1984).
[10]
PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530. X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at
"sesolution."; Jolles P., "An 88 amino acid long C-terminal sequence of human Powell M.J., Ogden J.E.; "Nucleotide sequence of human lactoferrin cDNA."; Nucleic Acids Res. 18:4013-4013(1990). X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) MEDLINE=99190892; PubMed=10089347; Acta Crystallogr. D 51:629-646(1995) TISSUE=Mammary gland; MEDLINE=90326549; PubMed=2374734; 253-->methionine mutant."; Biochemistry 36:341-346(1997). BBS Lett. 142:107-110(1982). SEQUENCE OF 3-711 FROM N.A. lactotransferrin."; Jolles P.; REAL THE REAL TO THE REAL TO THE REAL TO THE REAL THE REA

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A Williamorth G.K., Sommer J.R., Dasti S., Reddy M.K., Kanai A., Hotta Y.,
A Sugar J., Kunaramanickarel G., Munier F., Schorderet D.F.,
B Indri L., Iwata F., Kaier-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
Familial subspithelial corneal amyloidosis (gelatinous drop-like corneal dystrophy): exclusion of linkage to lactoferrin gene.";
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Corneal dystrophy: Exclusion of linkage to lactoferrin gene.";
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Corneal dystrophy: ARMSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FRARIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICKERONATE.
CORN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICKERONATE.
CORN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BINDING OF ANION, USUALLY BINDING OF ANION BAND CHARSE SOMEWHAT HIGHER DEGREES OF PREFERENCE INACOPERRONES THAN FOR MU-RECEPTORS, WHILE INACOPERRONES THAN FOR MU-RECEPTORS, WHILE WEDLINE=91166929; PubMed=1369293; Tani F., Iio K., Chiba H., Yoshikawa M.; "Isolation and characterization of opioid antagonist peptides derived Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus MEDLINE=99192677; PubMed=10089508;
Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker B.N.;
"Structure of human apolactoferrin at 2.0-A resolution. Refinement
and analysis of ligand-induced conformational change.";
Acta Crystallogr. D 54:1319-1335(1998). -!- SUBUNIT: MONOMER.
-: SUBCELLULAR LOCATION: Secreted.
-!- DOWAIN: COMPOSED OF TWO HOWOLOGOUS DOWAINS.
-!- DOWAIN: BELONGS TO THE TRANSFERRIN FAMILY. Agric. Biol. Chem. 54:1803-1810(1990). Acta Crystallogr. D 55:403-407(1999). X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) CHARACTERIZATION OF LACTOFERROXINS. EMBL; X53961; CAA37914.1; EMBL; U07643; AAB60324.1; EMBL; M93150; AAA36159.1; EMBL; M83202; AAA58551.1; EMBL; M83205; AAA58656.1; EMBL; M8422; AAA6665.1; EMBL; AF332168; AA46665.1; EMBL; BC015822; AAH15822.1; EMBL; M73700; AAA594791; EMBL; X52941; CAA37116.1; EMBL; V52941; CAA37116.1; EMBL; V95626; AAB57795.1; ---VARIANTS THR-30 AND ARG-48. Pubmed=9873069; from human lactoferrin." 1LFH; 31-OCT-93. 1LFI; 31-OCT-93. 1LGB; 31-AUG-94. 08-MAR-96. 1LCF; 31-AUG-94 1LCT; 31-OCT-93 1LFG; 31-JUL-94 S11228; 1LGC; 1BKA; 1DSN; 1HSE; 1VFD; PIR; PDB; PDB; PDB; PDB; 

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TRFL CAPHI STANDARD; PRT; 708 AA. Q29477; Q29479; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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66.7%; Pred. No. 0.21;
ttive 1; Mismatches
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708 AA;
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                                                                                                                                                                                                                                     Camelus dromedarius (Dromedary) (Arabian camel).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                                                                                                                 STRAIN-Somali, TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
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InterPro; IPR011156; Transferrin.
Pfan; PF00402; transferrin; 2.
PRINTS; PR00402; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
PROSITE; PS00205; TRANSFERRIN.
PROSITE; PS00207; TRANSFERRIN.
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            Score 65; DB 1; Length 711; Pred. No. 0.00015; 0; Mismatches 1; Indels
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2001 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin)
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LACTOTRANSFERRIN
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EMBL; AF165879; AAF82241.1; -.
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Best Local Similarity 91.7
Matches 11; Conservative
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Capra hircus (Goat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Caprinae; Capra.
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304 G -> A (IN REF. 2).
494 LLS -> P (IN REF. 2).
506 L -> F (IN REF. 2).
609 A -> P (IN REF. 2).
612 A -> P (IN REF. 2).
77211 MW, 080C175A0B69D430 CRC64;
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
BY SIMILARITY.

BY SIMILARITY.

IRON 1 (BY SIMILARITY).

IRON 1 (BY SIMILARITY).

IRON 1 (BY SIMILARITY).

IRON 2 (BY SIMILARITY).

IRON 3 (BY SIMILARITY).

IRON 6 (BY SIMILARITY).

ANION (BY SIMILARITY).

N-LINKED (GLCNAC. ..)

N-LINKED (GLCNAC. ..)
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MILA DROME STANDARD; PRT; 292 AA.

09XZL8; 09V391;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nebula protein.
NEAUR SCG6072.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophila.
NUSD TAXID=7227;
                                                                                                                                                                    SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                           Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
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-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Parm; PR00465; Transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
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EMBL, X78902, CAA55517.1; -.
HSSP; O77698; ICE2.
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RK STRAIN-BEFKELEY,

RM MININS-2019606; PubMed=10731132;

RM MADLINS-2019606; PubMed=10731132;

RA Adams N D. Celniker S.E., Holt R.A., Bobarner M., Henderson S.N.,

RA Adams N D., Celniker S.E., I.I. P.W., Hoskins R.A., Galle R.F.,

RA Adams N D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Worten J.R., Pandell M.D., Zlang Q., Chen L.X.,

RA Anton R.C., Ragers Y.H.C., Blazel R.G., Change M., Pfeiffer B.B.,

RA Abril J.F., Apdayani A., An H.-J., Andrews-Flemnkoch C., Baldwin D.,

RA Ballow R.W., Benes P.V., Berman B.P., Bhandari D., Beasley E.W.,

Ballow R.W., Benes P.V., Berman B.P., Bhandari D., Bolshkov S.,

Burtis K.C., Busan D.A., Buller H., Cadieu E., Center A., Chadra I.,

RA Burtis K.C., Busan D.A., Buller H., Cadieu E., Center A., Chadra I.,

RA Burtis K.C., Busan D.A., Ballke C., Davamport L.B., Davies P.,

RA Burtis K.C., Busan D.A., Balke C., Davamport L.B., Davies P.,

RA Burtis K.C., Busan D.A., Balke C., Davamport L.B., Davies P.,

RA Burtis K.G., Gabrilan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Li Z., Gan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Li Z., Mang J.M., Matton D.L.,

RA Harris N.L., Mattel B., McInted G.H., Wie M.-H., I Degwar C.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Rainer K., Remington K.A., Nelson D.C., Scheeler F., Shen H.,

Spier E., Spradling A.C., Stapleton M., Stupsk M.P., Shen H.,

Shier E., Spradling A.C., Stapleton M., Stupsk M.P., Shen H.,

RA Shier E., Starden G.H., Warney K.C., Wu D., Yang S., Yao Q.A.,

RA Shier E., Spradling A.C., Stapleton M., Stupsk M.P., Shen H.,

RA Shier E., Starden G.H., Warney K.C., Wu D., Yang S., Yao Q.A.,

RA Shier E., Starden G.H., Warney K.C., Wu D., Yang S., Yao Q.A.,

RA Shier E., Starden G.H., Warney B., Wang S., Yao Q.A.,

RA Shier E., Zhong F.N., Zhong W., Wang S., Zhu X., Shen H.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75991 MW;
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Matches 7; Conservative
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695 AA;
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                              rissum=Uterus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resolution.";
J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OP AN ANION, USUALLY BICARBONATE.
-!- SUBUNIT: MONOMER.
-!- SUBCELLUTAR LOCATION: Secreted
-!- SUBCELLUTAR LOCATION: Secreted
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                              Eŭkaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB, 1B72, 02-FEB-99.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin.
PPfam; PF00405; transferrin.
SMART; SM00094; TR FER; 2.
SMART; SM00094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 3; 1.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.
NON TER < 1 6
SIGNAL <1 6
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                                                                                                   59.7%; Score 40; DB 1; Length 292; 54.5%; Pred. No. 2.6; 24.5%; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Paramasivam M., Sinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                             EMBL; AF147700; AAD33987.1; -.
EMBL; AE003712; AAF52885.1; -.
FYBRS: PSGN0026629; nla.
SEQUENCE 292 AA, 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment)
                                                                                                                                                                                                                                                                 695 AA
   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
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                                                                                                                                6; Conservative
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                                                                                                   Query Match
Best Local Similarity
Matches 6; Conservat
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150 FQWLRSFRRLR 160
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Gaps
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"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . .) (POTENTIAL)
0.7B884D50E1845D CRC64;
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
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SEQUENCE
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                                                                                                                                                        Liu Y., Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885(1991).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
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IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (POTENTIAL).
ANION (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .)
R- IROG (IN REF. 1).
R -> Q (IN REF. 2).
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MGD, MG196837, Ltf.
InterPro; IPR001156, Transferrin.
PRINTS, PR00425; Transferrin, 2.
PRINTS, PR00405; TRANSFERRIN.
PROSTTE; P800205; TRANSFERRIN.
PROSTTE; P800206; TRANSFERRIN.
PROSTTE; P800206; TRANSFERRIN.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
            Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            -!- STBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN.
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                                                                                    SEQUENCE OF 1-14 FROM N.A. MEDLINE=9204209; PubMed=1939212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, J03298; AAA40525.1; -.
EMBL, D885.0; BAA13633.1; -.
EMBL, BC006904, AAH06904.1; -.
EMBL, M74778; AAA39427.1; -.
PIR, A28438; A28438.
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-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INFO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.

-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Planet P., dagoueix S., Bove J.M., Garnier M.; "Detection and characterization of the African Citrus Greening Liberobacter by amplification, cloning and sequencing of the rplKAJL-rpoBC operon.";
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-!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA' CHAIN.
-!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-NOV-1995 (Rel. 40, Last annotation update)
1016-0CT-2001 (Rel. 40, Last annotation update)
1018-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
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                                                                                                                                                                                                   Score 39, DB 1, Length 707, Pred. No. 9.6;
1; Mismatches 4; Indels
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InterPro; IPR001572; RNA_pol_B.
PFAM; PF00562; RNA_pol_B; 1.
PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
NON_TER 146 146
SEQÜENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
M -> L (IN REF. 2).
S -> T (IN REF. 2).
A -> D (IN REF. 1).
E -> G (IN REF. 1).
L -> V (IN REF. 1).
W, F26AE0340A4C19A8 CRC64;
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82
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Similarity 54.5%;
6; Conservative
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SEQUENCE FROM N.A.
STRAIN=Nelspruit;
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les 6; Conserv
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Best Local Similarity
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SEQUENCE FROM N.A. (A*3401/A*3402).
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DYNEIN HAS ATPASE ACTIVITY.
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1852 CFQWQSQLRYIQ 1863
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2017 204
3106 316
3133 342
3648 372
3648 372
1919 192
2530 223
2879 288
4568 AA;
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                                                                                                                                                                                          Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Cell Sci. 107:635-644 (1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitchell D.R., Brown K.S., "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
ODA4 OR ODA-4 OR SUP1.
Eukaryota, Varidiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomona dacaee; Chlamydomonadacaee; Chlamydomonadacaee; Chlamydomonadacaee; Chlamydomonadacaee; Chlamydomonadacaee; Chlamydomonadacaee; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- COFACTOR: FAD (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 235602; CAA846/1...,
WormPep; R13G10.2; CE25088.
InterPro; IPR002937; Amino_oxidase.
Pfam; PF01593; Amino_oxidase; L
Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
Hypothetical protein; Oxidoreductase; Plavoprotein; FAD.
311 366
                                                                                                                                                                                                                                                                                                                                                                                                                          Gardner A.E.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Durbin R.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                        TNR2 CAEEL STANDARD; PRT; 783 AA. 021988. (Rel. 37, Created) 15-DBC-1998 (Rel. 37, Created) 15-UNA-2002 (Rel. 41, Last sequence update) 15-UNA-2002 (Rel. 41, Last amnotation update) Hypothetical protein R13G10.2 in chromosome III. 13G10.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
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Best Local Similarity 50.0
Matches 6; Conservative
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540 CIDWGRDDRKVK 551
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SEQUENCE PROM N.A.
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YHB CHLRE
D DYHB CHL
C Q39555;
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Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
du Toit E.D., Parham P.;
"Structural diversity in the HLA-A10 family of alleles: correlations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (A*3401/A*3402).
MADLINES-93056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
"Distinctive HiA-A.B aningens of black populations formed by interallelic conversion."
   (ALPHA, BETA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1A34 HUMAN STANDARD; PRT; 365 AA.
P30453; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34(A-10) alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLED COLL (POTENTIAL).
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0
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Interpro, IPR04273, Dynein, heavy.
Pfam; PF03028; Dynein, heavy. 1.
Motor procein, Microtubules, Dynein, ATP-binding, Flagella,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 4568;
-!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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519961 MW; 9A9A5393C7C36AE7 CRC64;
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ATP (POTENTIAL)
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Pred. No. 95;
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Myxoma virus (strain Lausanne).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
             01-OCT-1989 (Rel. 12, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Serine proteinase inhibitor 1 (Serpin 1) (Serp-1)
SERPI OR M008.1L.
                                                                                                                                   Leporipoxvirus.
NCBI_TaxID=31530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | N-LINKED (GLCNAC, N-LINKED) | BY SIMILARITY) | N-LINKED (GLCNAC, N-LINKED) | GLCNAC, N-LINKED (GLCNAC, N-LINKED) | N-LINKED 
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AW-34 (A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                  MICROGLOBULIN).
-!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
(AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
               Tissue Antigens 41:72-80(1993).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 18; 2; Indels
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; Ig MHC.
InterPro; IPR00103597; Ig_c1.
InterPro; IPR001039; MHC_I.
Pfam; PF001029; MHC_I:
Prodom; PF001050; MHC_I:
SMART; SM00407; IGc1; I.
SMART; SM00407; IGc1; I.
MHC I; I.
MHC I; Iransmembrane; Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   063BF63E6E6E01F6 CRC64;
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                                                                                                                                                                                                                                                                                                                 EMBL, X61704, CAA43873.1, -.
EMBL, X61705, CAA43874.1; -.
PIR, S16767, S16767.
PIR, S16771, S16771.
HSSP, O19673, 1HSB.
MIM, 142800.
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66.7%;
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Best Local Similarity
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                                                                                                                                         A*3401.
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DOMAIN
TRANSMEM
DOMAIN
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DISULFID
DISULFID
VARIANT
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=91049428; PubMed=2173255;
Upton C., Macen J.L., Wishart D.S., McFadden G.;
Upton C., Macen J.L., Wishart D.S., McFadden G.;
"Myxoma virus and malignant rabbit fibroma virus encode a serpin-like protein important for virus virulence.";
Virology 179:618-631(1990).
                                                                                                                                                                                                                                                                            repeats of Shope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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SEQUENCE FROM N.A.

MEDLINE=87030884; PubMed=3021526;

Whon C., Carrell R.W., MoFadden G.;

"A novel member of the serpin superfamily is encoded on a circular plasmid-like DNA species isolated from rabbit cells.";

FEBS Lett. 207:115-120(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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3 319 320 REACTIVE BOND (BY SIMILARITY).
1 16 MKYLVLVLCLTSCACR -> MFNVVRV (IN
                                                                                                                                                                                                                         MEDLINE=87064296; PubMed=3023828; Upton C., McFadden G.; Upton C., McFadden G.; McFadden G.; McFadden G.; Upton C., McFadden G.; Ethorse thomology between the terminal inverted repeate fibrowa virus and an endogenous cellular plasmid species."; Mol. Cell. Biol. 6:265-276(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 369;
Pred. No. 18;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ND 3).
RDB31CE131C218A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, M35233; AAA46629.1; -.
EMBL, M12333; AAA81567.1; -.
EMBL, AF170726; AAF15055.1; -.
EMBL, AF170726; AAF14896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 AA; 41556 MW;
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PIR; B36418; B36418.
HSSP; P05121; B36418.
InterPro; IPR000215; Serpin.
Pfan; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative C
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369 AA

RESULT 11 SPI1\_MYXVL ID \_SPI1\_MYXVL

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                                                                                                                                                           SEQUENCE FROM N.A. MADAGE 8386274; MED. Tao H., Chen G.-M.; MADACKOW E.R., WARTHON-ECKETT R., Fay M.E., Tao H., Chen G.-M.; "Identification and baculovirus expression of the VP4 protein of the
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=MB4 / JCM 11007,

MEDLINE=21992816; PubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.

Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

-! SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSCMAL PROTEINS.
                                                                            Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
Viruses, dsRNA viruses, Reoviridae, Rotavirus.
                                                                                                                                                                                                                                          human group B rotavirus ADRV.";
Vixol. 67:2730-738(193).
-!- SUBCELLULAR LOCATION: Obter capsid.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis.
acteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacter.
NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 749;
Pred. No. 36;
0; Mismatches 6; Indels
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N-LINKED (GLCNAC. . .) (Po
D1223527DEAE0F21 CRC64;
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(GLCNAC.
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15-UUN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
N-LINKED
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N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, M91434; AAA47338.1; -.
InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 CFTWDMNCANVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWXRNMRKVR 12
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749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                      Viruses; dsRNA vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
RL28 THETN
ID RL28 THETN
AC Q8R9UI;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Mobn / Nigg;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shor C., Gill S.R., Heidelberg J.F.,
White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Bisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae AR39.",

Nucleic Acids Res. 28:1397-1406(2000).

-!-CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
diphosphate + L-histidyl-tRNA(His).

-!-SUBUNIT: HOWODINER (BY SIMILARITY).

-!-SUBCELLULAR LOCATION: Cytoplasmic.

-!-SUBLARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50862; AA TRNA LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Histidyl-tRNA synthetase (SC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.7%; Score 36; DB 1; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 AA; 48939 MW; 9CF859ED0E689DDF CRC64;
                                                                                                                                                                                                                                                                                     Chlamydia muridarum.
Bacteria, Chlamydiales, Chlamydiaceae, Chlamydia.
                                                                                                                                          428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  749 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.4%; Pred. No. 21; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001106; AAtRNA_ligaseII.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004516; Hiss-
InterPro; IPR004516; Hiss-
InterPro; IPR005314; tRNA-synt_2b.
Pfam; PF00387; tRNA-synt_2b; I.
Pfam; PF03129; HGTP_anticodon; I.
TIGRPAMS; IIGR00442; Hiss; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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P4_ROTGA STANDARD;
C Q04916;
T 01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE002349; AAF39630.1; -. HSSP; 032422; 1QE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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                                      235 WIRNMRK 241
4 WXRNMRK 10
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HISS OR TC0830
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                                                                                                                                        SYH CHLMU
Q9PJJ9;
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Matches

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Gaps

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(POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL)

(POTENTIAL)

(POTENTIAL) (POTENTIAL) (POTENTIAL)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92074218; PubMed=1962437;
MEDLINE=92074218; PubMed=1962437;
Dzianott A.M., Bujarski J.J.;
Dzianott A.M., Bujarski J.J.;
Mither nucleotide sequence and genome organization of the RNA-1 segment in two bromoviruses: broad bean mottle virus and cowpea chlorotic mottle virus.";
Virology 185:553-562(1991).
- - FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUJ-1993 (Rel. 26, Created)
01-JUJ-1993 (Rel. 26, Last sequence update)
01-JUJ-1993 (Rel. 40, Last annotation update)
1A protein [Includes: Helicase; Methyltransferase].
Broad bean moftle virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: TO 1A PROTEIN FROM CCMV, CMV, PSV AND TAV.
                                                                                                                                                                                                                                                          Score 35; DB 1; Length 62;
Pred, No. 4.6;
2; Mismatches 2; Indels
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                                                                                                                                                                                                   Ribosomal protein, Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
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InterPro; IPR002589; V methyltransf.
InterPro; IPR000606; Viral_helicasel.
Pfan; PP01443; Viral_helicasel; I.
Pfan; PF01660; Vmethyltransf; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                EMBL; AE013107; AAM24713.1; -.
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                                                                                                                                                                                                                                                                52.2%;
60.0%;
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              3 QWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                      27 RWKPNIRKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bromovirus.
NCBI_TaxID=12301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q00<u>0</u>20;
01-JUL-1993
01-JUL-1993
16-OCT-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIA BBMV
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VIA_BEMV
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1 CFQ----WXRNMRKV 11

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Db 347 CFKENKDWTENMRSV 361
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Search completed: February 21, 2003, 07:51:36 Job time : 6.2093 secs

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Q96m21 homo sapien Q96m21 homo sapien Q94p73 yaba monkas Q94b78 yaba monkas Q94b76 mus musculu Q91it1 mus musculu Q91it1 mus musculu Q91it1 mus musculu Q91it1 mus musculu Q91it2 lumpy skin Q94k87 zam maya (m Q94887 zam maya (m Q94g0 human immun Q9yqco human immun Q9yqco human immun Q9yqco human immun Q9yqsh human immun Q9yyli7 human immun Q9yyli8 drosophila
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Q9d4x5 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ©9UCYS;

01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

11-JUN-2001 (TrEMBLrel. 17, Last annotation update)

12-ctoferrin homolog (Fragment)

Homo sapiens (Human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB=PROSTATE;
Straumberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022347; AAH22347.1; -.
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                     Q9HPA3
Q9V346
Q9XFD5
Q9YQC0
Q9YQB9
Q9YJ17
Q9YJ17
Q9YJ17
Q9YJ17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                            Q8XSE2
Q9QB73
Q9DAJ3
                                                                                         Q9JIT1
Q91MQ5
Q9DHK5
P96223
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08S487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
PRELIMINARY;
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Q8TCD2
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Q9UCY5
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Q8TCD2
셤
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Q9u4m9 leishmania
Q9fhi9 arabidopsis
Q8655 erx2 conver
O81653 hemerocalli
Q9sic0 arabidopsis
Q77855 human immun
Q77856 human immun
Q97857 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q82462 salmonella
Q9xhpl sesamum ind
O31090 rhizobium l
Q93780 caenorhabdi
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Q9ucy5 homo sapien
Q9tr80 ovis aries
                                                                                                     February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds (without alignments) 114.078 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQTCD2
QQTCY5
QQTCY5
QQXHP1
QQXHP1
QQX3780
QQXXA3
QQXXA3
QQXXA3
QQXXA3
QQXXA3
QQYXA3
QQYXA3
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QQXXQX
QQX
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Gapop 10.0 , Gapext 0.5
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sp_numan:*
sp_numan:*
sp_namal:*
sp_namal:*
sp_organelle:*
sp_plant:*
sp_lant:*
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sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
sp_fungi:*
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67
1 CFQWXRNMRKVR 12
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length: 2000000000
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Perfect score:
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Maximum DB seq
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Bentley S.D., Holden M.T.G., Sebaihia M.
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Best Local Similarity
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nes 7; Conserv
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MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                          Sato I.;
"Characterization of the 84-kDa protein with ABH activity in human seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P07788; 1BKA.
InterPro; IPRO01156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovis aries (Sheep).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprine, Ovis.
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Salmonella.
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          Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.6%; Score 56; DB 4; Length 38; 90.9%; Pred. No. 0.00085; rive 0; Mismatches 1; Indels
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MEDIANE=95127729; PubMed=7827104;
MEDIANE=95127729; PubMed=7827104;
Gian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
HSSP, 077698; ICE2.
InterPro, IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-WAR-2002 (TYEMBLrel. 20, Last sequence update)
1-WAR-2002 (TYEWBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 AA
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                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 FOWORNMRKVR 31
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Matches 10; Conserv
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Q9TRB0;
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STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
"Molecular cloning of 11S globulin and 28 albumin, the two major seed storage proteins in sesame.";
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Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J., Feltwell T., Hamin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Moule S., O'Gaora P., Parry C., Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 albumin.
Sesamum indicum (Oriental sesame) (Gingelly).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
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01-57N-1998 (TrEMBLrel. 05, Last sequence update)
01-07T-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 31.0 kDa protein.
Hypothetical 31.0 kDa protein.
Rhizobium leguminosarum (biovar viciae).
Bacteria, Proteobacteria, alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                  Nature 413:848-852(2001).
EMBL, AL671276, CAD06049.1, -.
Hypothetical protein; Complete proteome.
SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Agric. Food Chem. 47:4932,4938(1999).

EMBL; AF091841; AAD42943.1; -.

InterPro; IRR003612; AAI.

InterPro; IRR001768; Try/amyl_inhbtr.

PRam; PF00234; tryp alpha_amyl; 1.

PRINTS; PR00499; AAI. 1.

SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.2%; Score 41; DB 16;
58.3%; Pred. No. 9.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                    STRAIN=129XI/SVJ;

BEDLINE=21676859;

Rodriguez I., Del Punta K., Rothman A., Ishii T., Mombaerts P.;

"Multiple new and isolated families within the mouse superfamily of
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Ravel C., Dubessay P., Blaineau C., Lignon M.-F., Bastien Bodet J.-P., Pages M.;
Leishmania major chronosome 5 complete sequence.";
Leishmania major chronosome 5 complete sequence.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; AF163772; AAF14642.1;
InterPro; IPRO2403409; MORN.
Fram; PF02493; MORN; 4.

SEQUENCE 415 AA; 46701 MW; 3E3AD710BF23691E CRC64;
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Pred. No. 20;
1; Mismatches 2; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DNA, chromosome 5, Pl clone.MFC19.
Arabidopsis thaliana (Mouse-ear cress).
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                              Nat. Neurosci. 5:134-140(2002).
EMBL; AY065506; AAL47911.1; -.
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                         Vir vomeronasal receptors.";
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                      NCBI_TaxID=10090;
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Q9U4M9;
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Q9U4M9
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                             "Structural and functional organization of the exopolysaccharide biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39."; Mol. Biol. (Mosk) 32.797-804 (1998). EMBL; AF028810; Az888911.; -. Hypothetical protein. SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;
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Ksenzenko V.N.;
                                                                                                           Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.7%; Score 40; DB 2; Length 273; 60.0%; Pred. No. 8.1; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C.elegans: A platform for investigating biology."; investigating biology."; science 282:2012-2018(1998). EMBL, Z81089; GAB03137.1; -. SEQUENCE 275 AA, 31716 MW; 9D69524FFC704DB2 CRC64;
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58.2%; Score 39; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 3; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                       STRAIN=VF39;
MEDLINE=99113394; PubMed=9914965;
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SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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01-JUN-2002 (TrEMBLrel. 21, C;
01-JUN-2002 (TrEMBLrel. 21, L;
01-JUN-2002 (TrEMBLrel. 21, L;
Vomeronasal receptor VIRE6.
VIRS6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.00,
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| ||:||:|
245 RWLRNLRKLR 254
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SEQUENCE FROM N.A.
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                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=387;
                                                                                   STRAIN=VF39;
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Nature 402:761-768(1999).
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STRAIN-CV. COLUMBIA;
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501 QWFRNMKK 508
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Q77855
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STRAIN=COLUMBIA; PubMed=10470850; MEDINE=9393451; PubMed=10470850; MEDINE=9393451; PubMed=10470850; Makamura Y., Asamizu E., Kotani H., Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H., Miyajima N., Tabata S.; Sirotural analysis of Arabidopsis thaliana chromosome S. IX. Sequence features of the regions of 1,011,550 bp covered by seventeen Pl and TAC clones."; Pl and TAC clones."; Parabidopsis thalistop and the second second
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                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hemerocallis hybrid cultivar.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales,
Hemerocallidaceae, Hemerocallis.
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                                                                                                                                                                                                                                                                                                      Indels
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Senescence-associated protein 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TYEMBLrel. 21, Created) 01-JUN-2002 (TYEMBLrel. 21, Last sequence update) 01-JUN-2002 (TYEMBLrel. 21, Last annotation update) Hypotherical 12.3 kDa protein.
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STRAIN=CV. STELLA D'ORO; TISSUE=SENESCING PETALS;
MEDLINE=99339248; PubMed=10412903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AA.
                                                                                                                                                                                                                                                                                                    1; Mismatches
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              389 CFNWLLKFRKLR 400
                                                                                                                                                                                                                                                                                                                                               1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                Best Local Similarity
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ID Q8SC55
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MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Mishman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 372;
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EMBL, AC007170; AAD25641.1; -
InterPro; IPR004264; Transposase_23.
Pfam; PPG0417 Transposase_23; 1.
SEQUENCE 531 AA; 60512 \( \text{MW} \); 57B3AC60C976A4B9 \( \text{CRC64} \);
Plant Mol. Biol. 40:237-248(1999).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
BMBL. AF082028; AAC34853.1, -.
PINTEPPO; IPR01128; CYTOCHROME_P450.
Pfam; PR00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
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Last annotation update)
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Q77855, 01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
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R Pams, Z47689; CAMSTR82.1; -. Rems, PF00516; GP120, 1.

R Pfam, PF00516; GP120, 1.

M AIDS, Coat protein; Glycoprotein.
                                                                                                                                                 Query Match 55.2%; Score 37; DB 15; Length 91; Best Local Similarity 60.0%; Pred. No. 9.9; Matches 6; Conservative 2; Mismatches 2; Indels
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Best Local Similarity 60.0%; Pred. No. 9.9;
Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 AA; 10530 MW; 8B10C62011F305D6 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
                                       Human immunodeficiency virus type 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
VCBI_TaxID=11676,
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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GenCore version 5.1.3  Copyright (c) 1993 - 2003 Compugen Ltd.  M protein - protein search, using sw model  Rebruary 21, 2003, 07:37:21; Search time 28.093 Seconds	S67. US-09-743-107B-89  SCOIE: 66  LADIE: BLOSUM62  Gapop 10.0 , Gapext 0.5	<pre>searched: 908470 seqs, 133250620 residues  Fotal number of hits satisfying chosen parameters: 908470  4inimum DB seq length: 0 4aximum DB seq length: 2000000000  Post-processing: Minimum Match 0%</pre>	A Geneseq_101002:*    SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1981.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1982.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1982.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1983.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1985.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1986.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1980.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA1990.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA2001.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA2001.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA2002.DAT:*   SIDSZ/gcgdata/geneseqy-embl/AA2002.DAT:*	Pred. No. is the number of results predicted by chance to he score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.  SUMMARIES  Query Score Match Length DB ID Descrip	1         65         98.5         12         21         AAY78074         Human lactoferrin           2         64         97.0         12         21         AAY78045         Human lactoferrin           4         64         97.0         12         21         AAY78046         Human lactoferrin           5         64         97.0         12         21         AAY78086         Human lactoferrin           6         64         97.0         12         21         AAY78099         Human lactoferrin           7         64         97.0         12         21         AAY78099         Human lactoferrin           9         64         97.0         13         21         AAY8048         Human lactoferrin           10         64         97.0         13         21         AAY78049         Human lactoferrin

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infection; inflammation; tumour; matory; anti-microbial; anti-tumour; Candida infection; fungicidal; altzer L, Dolphin GT; SEQ ID NO:74.

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                                                               AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to o specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food scuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used dinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 5.3e-05;
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                                             Claim 22; Page 35; 102pp; English
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as usinary tract infections, collife, and Candida infection on a mucosal membrane) inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Been though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections on a mucosal canbeauch), inflammations and/or tumours. The peptides can also be used on info stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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ANY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also thugicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used all inically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                              Score 64; DB 21; Length 12;
Pred. No. 7.9e-05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                       AAY78086 standard, Peptide, 12 AA.
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98SE-0002562.
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                                                                 Conservative
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                                                                                                                                  1 CFOWORNMRKVR 12
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                                               Similarity
                                                                                                   1 CFQWQRXMRKVR
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12 AA;
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 Sequence
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à d AAY78089 standard; Peptide; 12 AA

AAY78089

(first entry)

25-APR-2000

AAY78089;

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RESULT 7
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Query Match Best Local Similarity 100. Matches 12; Conservative

12 AA;

Sequence

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the direculation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urihary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food atuffs such as infant formula food. The peptides rea also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumou
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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100.0%; Pred. No. 7.9e-05;
live 0; Mismatches 0;
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                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:90.
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AAY78090 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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Matches 12; Conservative
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Synthetic.
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29-DEC-1998;
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                                           AAY78090;
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AAY78037
ID AAY78
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100.0%; Pred. No. 7.9e-05;
ive 0; Mismatches 0; Indels
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Claim 22; Page 37; 102pp; English.

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB.

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

36-JUL-1999; 06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

13-JAN-2000

WO200001730-A1

Homo sapiens. Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment or hrough the circulation. A medicinal product of the peptide or fragment or not be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Seen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower mable them to be used for the same purposes as lactoferrin at lower
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; burinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservativa
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative
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Best Local Similarity 91.7
Matches 11; Conservative
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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Dolphin GT

Baltzer L,

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food scuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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                                                                                                                                                                                                                           Dolphin GT
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                                                                                                                                                                                                                           Baltzer L,
                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 74; 102pp; English.
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                                                                                              99WO-SE01230.
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Matches 11; Conservative
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                              WO200001730-A1
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0; Gaps

Score 64; DB 21; Length 13; Pred. No. 8.6e-05; 0; Mismatches 1; Indels

97.0%; 91.7%;

13 AA;

(first entry)

99WO-SE01230.

06-JUL-1999;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary trace infections, collitis, and candida infections and membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also infood stuffs such as infant formula food. The peptides are also though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used dinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food, infant formula, anti-inflammatory, anti-microbial, anti-tumour,
urinary tract infection, colitis, Candida infection, fungicidal,
bactericidal, preservative.
                                                                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 8.6e-05;
0; Mismatches 1; Indels
                                                                                                         Dolphin GT
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                                                                                                        Baltzer L,
                                                                                                                                                                                                              Claim 18; Page 74; 102pp; English
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             98SE-0002441.
98SE-0002562.
98SE-0004614.
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98SE-0002562.
98SE-0004614.
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                                                                          (ASCI-) A+ SCI INVEST
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                                                                                                                                     WPI; 2000-147388/13
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17-JUL-1998;
29-DEC-1998;
             06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment or through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as unimary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower cannot be used for the same purposes as lactoferrin at lower
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                                                               New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
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Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                 Claim 12; Page 69; 102pp; English.
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98SE-0004614.
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nes 11, Conservative
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29-DEC-1998;
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1 Similarity 91.7%;
11; Conservative
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Best Local Similarity
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Matches
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                           AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or Fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food, infant formula, anti-inflammatory, anti-microbial; anti-tumour,
utinary tract infection, colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                           Score 64, DB 21; Length 14, Pred. No. 9.2e-05; 0; Mismatches 1; Indels
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Claim 15; Page 75; 102pp; English.
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91.7%;
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es 11; Conservative
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29-DEC-1998;
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urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant foormula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64; DB 21; Length 14;
Pred. No. 9.2e-05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-ulcer agent; low toxicity; stable; heat-resistant.
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ID AAY7
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Human lactoferrin derived peptide SEQ ID NO:35.
25-APR-2000 (first entry)
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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens Synthetic.

WO200001730-A1.

13-JAN-2000.

99WO-SE01230 06-JUL-1999; 98SE-0002441. 98SE-0002562. 98SE-0004614. 06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

(ASCI-) A+ SCI INVEST AB.

Baltzer L, Dolphin GT; Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 12; Page 69; 102pp; English.

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through accoderrin. The spetides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used allocated basis because of high production costs. Therefore, provision of peptides because of high production costs. Therefore, provision of peptides based on lactoferrin at lower

15 AA; Sequence

. 0 Query Match

97.0%; Score 64; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 9.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels

1 CFOWORXMRKVR 12

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4 CFOWORNMRKVR 15

Search completed: February 21, 2003, 07:56:43 Job time : 28.093 secs

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Sequence
Seq
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Sequence 3, Application US/08204487

Patent No. 5565425

APPLICANT: YAMADATION:

APPLICANT: YAMADATION:

APPLICANT: MAKASHIMA, HIDEKI

APPLICANT: TANARA, SHIGEAKI

APPLICANT: TANARA, SHIGEAKI

APPLICANT: TANARA, SHIGEAKI

APPLICANT: TOSAKO, SHUN'ICHI

APPLICANT: TOSAKO, SHUN'ICHI

APPLICANT: UCHIDA, TOSHIMA

ITILE OF INVENTION: UNBLI INFECTION AND PROLIFERATION

TILLE OF INVENTION: UNHIBITORS

WUMBER OF SEQUENCES: 8

CORRESPONDENCES: BATANT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT

STREET: 53 STATE STREET

CITY: BOSTON

STATE: MA

CONNTRY: USA

ZIP: 02109

COMPUTPP ...
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NAME.KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 0.2-MAR-1994
CLASSIFICATION: 514
ATTONEY AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/POCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 248-7100
INFORMATION POR SEQ ID NO: 3:
SEQUENCE CRARACTERISTICS:
LENGTH: 18 amino acids
TWENTER AMINOR AND ACIDS
TELENGTH: 18 amino acids
TELENGTH: 18 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-08-204-487-3
  Appl
Appl
Appli
Appli
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Appli
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                                                                                                                                                              February 21, 2003, 07:50:40; Search time 8.93023 Seconds (without alignments)
39.537 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25,
Sequence 4, P
Sequence 10,
Sequence 10,
Sequence 7, P
Sequence 8, P
Sequence 8, P
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Sequence 6,
Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7,
Sequence 3,
Sequence 5,
Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3,
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Sequence 25
Sequence 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*
. /cgn2 6/ptodata1/iaa/5A COMB.pep:*
. /cgn2 6/ptodata1/iaa/5B COMB.pep:*
. /cgn2 6/ptodata1/iaa/6A_COMB.pep:*
. /cgn2 6/ptodata1/iaa/6A_COMB.pep:*
. /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
. /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
. /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
                         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-755-161A-3
US-07-755-161A-3
US-08-256-771-25
US-08-256-771-25
US-08-21-984-24
US-08-21-984-25
US-09-508-734-4
US-09-508-734-4
US-09-508-734-6
US-07-755-161A-10
US-07-755-161A-10
US-07-755-161A-10
US-08-204-488-7
US-08-204-488-7
US-08-204-488-7
US-09-208-734-8
US-07-891-174-8
US-07-891-174-8
US-07-891-174-8
US-07-891-174-8
US-07-891-174-8
US-08-26-771-30
US-08-28-771-30
US-08-311-984-29
US-08-311-984-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                         262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                 M protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                        US-09-743-107B-89
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iinimum DB seq length: 0
laximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                        litle:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                   scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atabase:
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APPLICANT: YOUR MING LI
APPLICANT: ATHERN VLASSARA
APPLICANT: HELEN VLASSARA
APPLICANT: ATHORY CERMIT
TITLE OF INVENTION: BUDREDUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: SOFTED OF THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSE: Kauber & Jackson
ADDRESSE: Kauber & Jackson
ADDRESSE: Kauber & Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.0%; Score 64; DB 2; Length 18; Best Local Similarity 91.7%; Pred. No. 3.8e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                              Length 18;
                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack
STATE: 411 Hackensack
STATE: New Jersey
COUNTEY: USA
ZIP: 07601
COMPUTER REABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIIR Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                Score 64; DB 1; 1
Pred. No. 3.8e-05;
                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 947-1-008A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
CLASSIFICATION DATA:
PRICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGRAT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 86,742
REFERENCE/DOCKET NUMBER: 947-1-00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRANCE: 201 487-5800
                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08485948
Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sich.
TOPOLOGY: linea.
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 amino acids
                                                            Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
; OTHER INFORMATION:
US-08-204-487-3
                                                                                                                                                         1 CFQWQRXMRKVR 12
                                                                                                                                                                                                       CFOWORNMRKVR 12
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Gaps

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Parent No. 5891341

GENERAL INFORMATION:
APPLICANT: LI, YONG MING
APPLICANT: VIASSARA, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i; Indels
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE:
RAUGHER & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STREET: New Jersey
CUNTRY: USA
ZIP: 07601
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION S14
PRICR APPLICATION NUMBER: US/08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION NUMBER: 26,742
REPERBENCE/DOCKET NUMBER: 947-1008 CIP
TELECOMMUNICATION INFORMATION:
NAME: Jackson Esq., David A.
REPERBENCE: 201 487-5800
TELEFRAX: 201 343-1684
TELERY: 201 343-1684
TELERY: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHRACTERISTICS:
LENGTH: 18 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08475055; Patent No. 5962245; GENERAL INFORMATION:
Application US/08628380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: BUDPROD
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWORNMRKVR 12
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ORGANELLE:
IMMEDIATE SOURCE:
LIBBARY:
CLOME:
POSITION IN GENOME:
CHROMOSONE/SECHENT:
MAP POSITION:
UNITS:
FRATICS:
FRATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" sublication INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.0%; Score 64; DB 1; Length 20;
                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION NUMBER: US/07/755,161A
PRICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECHOWNICATION INFORMATION:
TELECHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
       OPERATING SYSTEM: MS-DOS
                                             DisplayWrite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 19
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-755-161A-3
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Patent No. 5304633
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10 Antimicrobial Agent NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STREET: U.S.A.
COUNTRY: U.S.A.
                                                                                                                                                                                          ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 64; DB 2;
Pred. No. 3.8e-05;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/485,948
FILING DATE: 08/48,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/48,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/48,217
FILING DATE: JUNE 7, 1995
CLASSIFICATION:
ATOONEY/AGENT INFORMATION:
NAWE: JACKSON ESG., DAVIG A.
REGISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-0
TELEPHONE: 201 497-5800
TELEFAX: 201 343-1684
TELEFAX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acid
STRANDENDESS: single
TYPE: amino acid
STRANDENDESS: single
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: internal JS-08-475-055-8
                                      ADDRESSEE: Klauber
STREET: 411 Hackens
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWORNMRKVR 12
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JS-07-755-161A-3
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 19"
FEATURE: NAME/KEX: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 19
LOCATION: OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" AUTHORS:
AUTHORS:
ATTHORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ANGAGHIMA, HIDERI
APPLICANT: MAKSHIMA, HIDERI
APPLICANT: MOSUCHI, MATARU
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: CHAMSAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIAKI
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.0%; Score 64; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.2e-05; Matches 11; Conservative 0; Mismatches 1; Indels
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COMPUTER READMELE FORM:

CMEDIUM TYPE: Floppy disk
COMPUTER: TEM FC compatible
CURRENT APPLICATION DATA:
FILING DATE: O2-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REPREBURS/COCKET NUMBER: FJN-019
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08204487; Patent No. 5565425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQRXMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                              TITLE:
JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-204-487-1
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                                                                 Gaps
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                                                                 Indels
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Sequence 3, Application US/07891174
Sequence 3, Application US/07891174
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: BO. C.
COUNTRY: U.S.A.
ZIP: ZO005
COMPUTER READABLE FORM:
MEDIUM TYPE: DisplayMrite
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DisplayWrite
COMPUTER: DisplayWrite
COMPUTER: DisplayWrite
CONTRY: DisplayWrite
CONTRY: DisplayWrite
CONTRY: DisplayWrite
SOFTWARE: DisplayWrite
CONTRY: DisplayWrite
CONTRY: DisplayWrite
CONTRY: APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTOREY AGENT THORWATION:
APPLICATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 31-8856
TELEPRAX: 202-371-8856
                                           Pred. No. 4.2e-05; ); Mismatches 1;
                                         Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITS:
FEATURE:
NAME/KEY: modified site
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INDIVIDUAL ISOLATE:
DEVELORMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL LIVE:
CRLL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                             1 CFQWQRXMRKVR 12
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CHROMOSOME/SEGMENT
MAP POSITION:
                                                                                                                                                    2 CFOWORNMRKVR 13
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FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: HYPOTHETICAL:
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US-07-891-174-3
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US-08-256-771-24
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US-08-381-984-24
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Sequence 24, Application US/08256771
Fatent No. $65650
Fatent No. $6650
Fatent No. $6600
Fatent No. $
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
LOCATION: 1..20
LOCATION: 1..20
LOTHER INPORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INPORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPERSINCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQRXMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.0%; Score 64; DB 1; 1
ilarity 91.7%; Pred. No. 4.2e-05;
Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                25.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                1 CFOWORXMRKVR 12
                                           2 CFQWQRNMRKVR 13
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                                                                    RESULT 9
US-08-256-771-25
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Sequence 4, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Sampang Genex Corporation
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism
TITLE OF INVENTION NUMBER: US/9/508,734
CURRENT FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 1999-07-13
NUMBER: KOPATEHINI 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment there
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . LOCATION:
. IDENTIFICATION METHOD:
. OTHER INFORMATION: /note= "cysteine residues at positions 2
. OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
. US-08-381-984-25
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                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM COMPATION:
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION NUMBER: US/08/381,984
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
TELEGATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INPORMATION:
TELEFAK:
TELEFAK:
TELEFAK:
TELEFAK:
TELEFAK:
TELEFAK:
TELEFAK:
TELEFAK:
                                                                                                     805 Fifteenth Street, N.W., #700
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.7
Matches 11, Conservative
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                                                                                    STREET: 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-508-734-4
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| OTHER INFORMATION: | And 19 are bonded by disulfide linkage" |
| OTHER INFORMATION: and 19 are bonded by disulfide linkage" |
| OTHER INFORMATION: | Anne/KEY: | |
| LOCATION: | LOCATION: | IDENTIFICATION METHOD: |
| OTHER INFORMATION: | Anne/KEY: |
| OTHER INFORMATION: | Poptides including the specified peptide as a fragment therec
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; Sequence 24, Application US/08381984
; Patent No. 2804555;
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Wachington
STATE: D.C.
COUNTY: U.S.A.
ZIP: 20005
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER LAUGH FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: In Compatible COMPUTER: In Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: APPLICATION: 252
PRIOR APPLICATION 1252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: APPLICATION NUMBER:
FILING DATE: ATOMANATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
UNMER OF SEQUENCES: 32
CORRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQRXMRKVR 12
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NAME/KEY:
LOCATION:
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PILING DATE:
ATTORNATION:
NAME:
NAME:
WATER M. Cheek Jr.
REGISTRATION NUMBER: 33 367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
02-07-755-161A-10
                                                                                                                                                                                     10:
                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10
SEQUENCE FRARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: modified site
LOCATION: 21
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NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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Best Local Similarity
Matches 11; Conserva'
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IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:
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                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: Useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT APPLICATION NUMBER: US/09/508,734
PRIOR PILING DATE: 1090-06-01
PRIOR PILING DATE: 1099-07-14
PRIOR PILING DATE: 1099-07-14
PRIOR FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
LENGTH: 24
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                                                                                                Ouery Match 97.0%; Score 64; DB 4; Length 22; Best Local Similarity 91.7%; Pred. No. 4.6e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
1S-07-755-161A-10
Sequence 10, Application US/07755161A
Sequence 10, Application US/07755161A
Sequence 10, Application US/07755161A
Settle No. 5304633
SPATILE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDERS: ADDRESS: ADDRESS: ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2006
STATE: D.C.
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DISPLAYMITE
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: 19910905
CLASSFICCATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSFICCATION DATA:
APPLICATION NUMBER:
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Best Local Similarity 91.7
Matches 11; Conservative
                   TYPE: PRT
CORGANISM: Homo sapiens
JS-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
IS-09-508-734-6
                                                                                                                                                                                                                   2 CFOWORNWRKVR 13
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JS-09-508-734-6
LENGTH: 22
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" AUTHORS:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21"
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IDENTIFICATION METHOD:
OFFER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS;
TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 1; Length 25;
Pred. No. 5.2e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 21, 2003, 08:04:26 Job time : 9.93023 secs
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JOURNAL:
SOLUME:
SSUE:
PAGES:
DATE:
PULING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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CLONE:
CLONESCAME/SEGMENT:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FRATURE:
MANAFAREY:
MANA
                                                           Sequence 10, Application US/07891174

Sequent No. 5317084

GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington STREET: 0.C.
COUNTRY: U.S.A.

ZIATE: 10.C.
COUNTRY: U.S.A.

MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
COMPUTER: DisplayWitte
CURRATION SYSTEM: MS-DOS
SOFTWARE: DisplayWitte
CURRATION SYSTEM: MS-DOS
SOFTWARE: DisplayWitte
CURRATION DATA:
APPLICATION NUMBER: US 07/755,161
PRILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION INFORMATION:
TELEPRAN: 202-371-8856
TELEPAN: 202-371-8856
TELEPAN: COS COLORS OF TO NO. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acidd STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: modified site LOCATION: 21
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HYPOTHETICAL:
HYPOTHETICAL:
ANTI-SERGE:
RAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL TYPE:
ORGANELLE:
ORGANELLE:
ORGANELLE:
IMMEDIATE SOURCE:
       RESULT 15
US-07-891-174-10
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Sequence 16, Appl Sequence 17, Appl Sequence 10, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 715, Ap Sequence 5715, Ap Sequence 7715, Ap Sequence 7715, Ap Sequence 7, Appli Sequence 2, Appli Sequence 48879, A Sequence 2, Appli Sequence 2, Appli Sequence 25, Appli Sequence 15, Appli Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 28, Appli Sequence 28, Appli Sequence 18, Appli Sequence 28, Appli

Sequence 4,

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97.0%; Score 64; DB 9; Length 15; 91.7%; Pred. No. 2.5e-05; cive 0; Mismatches 1; Indels
0 US-09-904-536:14

0 US-09-904-536-15

0 US-09-904-536-16

0 US-09-904-536-10

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US-09-798-869-15
US-09-798-869-11
US-09-798-869-10
US-09-798-869-28
US-09-798-869-24
US-09-798-869-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERCENT OF A PRICATION US/09798869
PUBLICATION NO. US20030022821A1
GENERAL INFORMATION
PAPPLICANT: USEN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEC ID NOS: 30
SEO THANKE: FASELEC FOR WINDOWS VEISION 4.0
SEO THANKE: PASELEC FOR WINDOWS VEISION 4.0
SEO THANKE: PASELEC FOR WINDOWS VEISION 4.0
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
     Matches 11; Conservative
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ORGANISM: HOMO SAPIENS
US-09-798-869-2
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Best Local Similarity
     US-09-798-869-20
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Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 22, Appli
Sequence 29, Appli
Sequence 30, Appli
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Sequence 3, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 9, Appli
                                                                                                                          February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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Sequence 1
Sequence 1
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| CGRL2 6 (prodata/2/pubpaa/USOB NEW PUB.pep:*
| CGRL2 6 (prodata/2/pubpaa/DCT_NEW FUB.pep:*
| CGRL2 6 (prodata/2/pubpaa/USOF_NEW FUB.pep:*
| CGRL2 6 (prodata/2/pubpaa/NEOF_PUBCOMB.pep:*
| CGRL2 6 (prodata/2/pubpaa/USOF_PUBCOMB.pep:*
| CGRL2 6 (prodata/2/pubpaa/USOF_NEW_PUB.pep:**
| CGRL2 6 (prodata/2/pubpaa/USOF_NEW_PUB.pep:***
| CGRL2 6 (prodata/2/pubpaa/USOF_NEW_PUB.pep:***
| CGRL2 6 (prodat
                     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-023-096-2
US-09-798-869-6
US-09-798-869-3
US-09-798-869-7
US-09-798-869-7
US-09-798-869-7
US-09-798-869-2
US-09-798-869-2
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US-09-798-869-2
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US-09-904-536-8
US-09-904-536-9
US-09-904-536-11
US-09-904-536-12
US-09-904-536-12
                                                                                                                                                                                                                                                                                                                                                              Potal number of hits satisfying chosen parameters:
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                                                                                         OM protein - protein search, using sw model
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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JULIOLATION OF APPLICATION US/09798869
| Sequence 6, Application US/09798869
| Publication No. US20030022821A1
| GENERAL INFORMATION:
| APPLICANT: JOHN SIGURD SYENDSEN
| APPLICANT: JOHN SIGURD SYENDSEN
| APPLICANT: BALDUR SYENDSEN
| TITLE OF INVENTION: BIOACTIVE PEPTIDES
| FILE REFERENCE: A34049-PCT-USA-A
| CURRENT APPLICATION NUMBER: US/09/798,869
| CURRENT FILING DATE: 1999-08-31
| PRIOR PELING DATE: 1999-08-31
| PRIOR PELING DATE: 1999-08-28
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: PRACECOL NUMBER: GERSHB938-4
| PRIOR FILING DATE: 1998-08-28
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: PRACECOL NUMBER: DESCRIPTION NUMBER: DESCRIPTION NUMBER: DESCRIPTION NUMBER: GERSHB938-4
| PRIOR FILING DATE: 1998-08-28
| NUMBER OF SEQ ID NOS: 30
| SEC ID NO 6 | LENGTH: 15
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OCHN SIGURD SURDERN
APPLICANT: WYETEIN REKUAL
APPLICANT: BALDUR SVEINBJ (RNSON)
APPLICANT: BALDUR SVEINBJ (RNSON)
APPLICANT: BALDUR SVEINBJ (RNSON)
APPLICANT: BALDUR SVEINBJ (RNSON)
TITLE OF INVENTION: BIOACTUR PEPTIDES
FURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PILING DATE: 1998-08-31
PRIOR PILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
        Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative (
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                       1 CFOWORXMRKVR 12
                                                                                                                                                                      22 CFOWORNMRKVR 33
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US-09-798-869-3
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LENGTH: 15
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Patent No. US20020160941A1

GENERAL INFORMATION:

APPLICANT: Kruzel, Marian L.

APPLICANT: Kurecki, Tomasz

APPLICANT: Gollnick, Paul D.

APPLICANT: Gollnick, Paul D.

APPLICANT: Gollnick, Paul D.

TITLE OF INVENTION: Cloning, Expression, and Uses of Human

TITLE OF INVENTION: Lactoferrin

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSE: Jacobson, Price, Holman & Stern

STERET: 400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.0%; Score 64; DB 9; Length 25; Best Local Similarity 91.7%; Pred. No. 4.1e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PLING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-34
PRIOR FILING DATE: 1998-08-36
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-GEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MX-1994
ATTORNEY/AGBNT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/F5916
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
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                                                                                                                                                                                                                                                                                                   SEQ ID NO 20
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Score 64; DB 9; Length 694;
Pred. No. 0.00096;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53; DB 9; Length 15; Pred. No. 0.0021;
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Best Local Similarity
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63.6%; Pred. No. 0.077;
iive 1; Mismatches
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63.6%; Pred. No. 0.12;
iive 1; Mismatches
                                                                                                                                                                                                               Sequence 4, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: BALDUR SVEINBJ(RNSCN)
AUTLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A4649-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-11
PRIOR FILING DATE: 1999-08-14
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FARESEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geguence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGHED SVENDERN
APPLICANT: ALLOW SIGHED SVENDERN
APPLICANT: ALLOW SUGIND (RNSON)
ITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 1090-09-19
PRIOR APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR PLILING DATE: 1998-08-31
PRIOR FILING DATE: 1208-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FREESED for Windows Version 4.0
SEQ ID NOS: 32
IENGTH: 25
TYPE: PRI
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity (
         1 CFQWQRXMRKV 11
                                                                 3 CYQWQWRMRKL 13
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CRGANISM: MURINE
US-09-798-869-4
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US-09-798-869-22
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      1; Indels
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Pred..No. 0.0034;
                                                                                                                                                                                                  RESULT 6
18-09-798-869-23
Sequence 23, Application US/09798869
Publication No. US2003002281A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: (YSTEIN RENDAL
APPLICANT: (YSTEIN RENDAL
APPLICANT: HALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: A34049-PCT-USA-A
CURRENT FILING DATE: 1999-003-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-003-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO SEQ
LENGTH: 25
   2; Mismatches
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Publication No. US2003002281A1
GENERAL INPORMATION.
APPLICANT: USTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: HALDUR SVENDSEN
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-32
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRACE FRACES OF UNION SEQ ID NO SEQ ID
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Best Local Similarity 72.7°
Best Local Similarity 72.7°
8; Conservative
                                                        1 CFOWORXMRKV 11
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                                                                                                                   3 CYOWORRMRKL 13
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ORGANISM: CAPRINE
IS-09-798-869-23
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IS-09-798-869-7
Matches
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Sequence 30, Application US/09798869
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; ORGANISM: BOVINE
US-09-798-869-30
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US-09-864-761-47985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.1%; Score 41; DB 9; Length 15; Best Local Similarity 63.6%; Pred. No. 0.26; Matches 7; Conservative 1; Mismatches 3; Indels
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                                                               GENERAL INFORMATION:
FILE PEFRENCE:
GURRENT FILING DATE:
FRIOR APPLICATION NUMBER:
FRIOR APPLICATION NUMBER:
FRIOR FILING DATE:
FRIOR FILING DATE:
FRIOR APPLICATION NUMBER:
GENERAL ING DATE:
FRIOR FILING DATE:
FRI
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: BALDUR SVEINBLEN
APPLICANT: BALDUR SVEINBLEN
APPLICANT: BALDUR SVEINBLEN
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: AJ4049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRESESE (FOR WINGOME Version 4.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Matches 6, Conserv
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US-09-798-869-29
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US-09-798-869-29
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RESULT 12 US-09-798-869-30

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Sequence 47985, Application US/09864761
| Patent No. US20020048763A1
| Patent No. US20020048763A1
| Patent No. US20020048763A1
| Patent No. US20020048763A1
| APPLICANT: Rank, David R. APPLICANT: Rank, David R. APPLICANT: Hanzel, David R. APPLICANT: Corn, Weshberg GRNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITTLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY APPLICANT: GENE EXPRESSION ANALYSIS BY MICROARRAY CORRENT APPLICANTON NUMBER: US 00/20/466
| PRIOR PRIOR TILING DATE: 2001-05-23 |
| PRIOR APPLICATION NUMBER: US 60/180/312 |
| PRIOR APPLICATION NUMBER: US 60/20/456 |
| PRIOR PRING DATE: 2000-06-26 |
| PRIOR PRING DATE: 2000-06-26 |
| PRIOR PRING DATE: 2000-06-30 |
| PRIOR PRING DATE: 2000-06-30 |
| PRIOR PRING DATE: 2001-01-30 |
| PRIOR PRILING DATE: 2001-01-30 |
| PRIOR PRILICATION NUMBER: PCT/US01/00665 |
| PRIOR PRILING DATE: 2001-01-30 |
| PRIOR PRILING DATE: 2001-01-30 |
| PRIOR PRILICATION NUMBER: PCT/US01/00665 |
| PRIOR PLILOR DATE: 2001-01-30 |
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Pred. No. 0.26;
3; Mismatches
                                                     APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCE: A34049-PCT-USA-A
CURRENT FILICATION NUMBER: US/09/798,869
CURRENT FILICATION NUMBER: COT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-18
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FSELSEQ for Windows Version 4.0
SSENGTH: 15
Publication No. US20030022821A1 GENERAL INFORMATION:
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54.58;
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Best Local Similarity 54.5
Matches 6; Conservative
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Deficial Involvations:
APPLICANT: Barry III, Clifton E.
APPLICANT: Barry III, Clifton E.
APPLICANT: DeBarber, Andrea E.
APPLICANT: DeBarber, Linda-Gail
APPLICANT: Bekker, Linda-Gail
APPLICANT: Berkerente of Halth and Ruman Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFRENCE: 015204131000S
CURRENT APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGHH. 489
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OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
15-09-888-320-2
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUE 1.00e-06
IS-09-864-761-47985
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Pred. No. 1.8;
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                                                          PRIOR FILING DATE: 2001-01-30, PRIOR PILING DATE: 2001-01-30, PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 47985
LENGTH: 21
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2001-01-30
NITMBER: PCT/US01/00670
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Publication No. US20030013090A1
GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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ORGANISM: Homo sapiens
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16 CFQWRR 21
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JS-09-888-320-2
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Sequence 8, Application US/09904536 Patent No. US20020111475A1 GENERAL INFORMATION:

ESULT 15 IS-09-904-536-8

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ALFULCANT: McGrew, Jeffrey T.

TITLE OF INVENTION: PLT3-L MUTANTS AND METHODS OF USE
FILER REFERENCE: 03260.028

CURRENT APPLICATION NUMBER: US/09/904,536

PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100

PRIOR PLING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 20

CORTANDE: PATENTING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 20

CORTANDE: PATENTING SAPING

SOFTWARE: PATENTING SAPING

CORTANDES: PATENTING

NORTHER OF SEQ ID NOS: 20

CORP. MATCH SEQ ID NOS: 20

CORS. MATCH SEG ID NOS: 20

CORS. MATCH SEG ID NOS: 20

CORS. MATCH SEG ID NOS: 20

NATHER OF SEG ID NOS: 20

NATHER OF SEG ID NOS: 20

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OF TOROWANTER 187

Search Completed: Pebruary 21, 2003, 08:11:55

JOB time: 6.88372 secs
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Copyright (	earch,	. 21,	-09-743-107B CFQWQRXMRKVR	0.0	Beds,	atisfying	2000000000	ım Match ım Match ıg first	* * * * *	or or	1.0 1.0 1.0 1.0 1.0	- 1	711	~ 1	4568 275	932 206	206	289	515 543	1135	121	433	4 8 9 4 8 9	23.5	275	4, 4, 6, 7, 6, 7, 7, 7,	1391	1 H C	3
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fprA protein - Myx	hypothetical prote	cell cycle arrest	ornithine decarbox	probable cytochrom	cytochrome P450-li	cytochrome P450 ho	cytochrome P450-li	cytochrome P450 mo	hypothetical prote	hypothetical prote	finger protein unk	hypothetical prote	kinase-related pro	protein F21H11.2 [	carcinoembryonic a
T10126	AD2346	A39654	S52784	B96691	B85441	T04730	C85441	T52174	AB0858	T24218	842526	D83181	A35774	D88450	D33876
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270	298	306	435	481	492	499	200	200	511	536	614	1746	2594	2700	114
53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	51.5
35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	34
30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	4.5

Gaps

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NyAlternate names: lactotransferrin
Cispecies: Mus musculus (house mouse)
Cjate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CjAccession: A28438; A41205
R;Pentecost, B.T.; Teng, C.T.
R;Pentecost, B.T.; Teng, C.T.
A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretine in house number: A92596; MUID:87280033; PMID:3611056
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A,Residues: 3.707 CPEN>
A,Cross-references: EMBL.J03298
R,Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A,Fitle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A,Reference number: A41205, MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
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Fill9/Domain: signal sequence #status predicted <MAT>
Fill0-707/Product: lactotransferrin #status predicted <MAT>
Fill8-655/Domain: transferrin repeat homology <TRH2>
Fill94/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 3.6;
1; Mismatches 3; Indels
                                   DB 2; Length 708; 0.083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Oian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Flat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A.THLE: Isolation and characterization of sheep lactoferrin,
A; Reference number: $52107; WUID:95127729; PMID:7827104
A; Accession: $52107
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A;Molecule type: protein
A;Residues: 1.33 Q1AA
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
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A,Molecule type: DNA
A,Residues: 1-15 <LIUD.
A),TCOS = Ferences: GB M74778
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
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Pred. No. 0.016;
                                                                                                                             2; Mismatches
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Best Local Similarity 63.0
Lea 7; Conservative
                                        Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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(Superfamily: transferrin; transferrin repeat homology

(S. Warders) 
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Niversely, V.S. Nocart, M.; Guerin, G.; Martin, P.

Nichen Biophys. Res. Commun. 203, 1324-1332, 1994

Nititle: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A; Reference number: JC2323, MUID:94380447; PMID:8093048

A; Reference number: JC3223

A; Molecule type: mRNA

A; Residues: 1-708 < LEP>
C; Superfamily: transferrin; transferrin repeat homology
C; Superfamily: transferrin; glycoprotein
F; S59-696, Domain: transferrin repeat homology < TRH2>
F; 252, 300, 387, 495, 564/ Binding site: carbohydrate (Asn) (covalent) #status predicted
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mE A;Reference number: S07160, MUID:88001031; PMID:3477300
A;Accession: S07160
A;Accession: S07160
A;Nolecule type: mRNA
A;Residues: 436-487, 'A', 489-711 <RAD>
A;Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
B;Panella, T.U.; idu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyth A;Reference number: A61169; MUID:91235214; PMID:1674448
A;Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A;Note: this is the final paper in a series
R;Houen, G; Hoegdall, E.V.; Barkholt, V; Norskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A;Title: Lactocherrin: similarity to diamine oxidase and purification by aminohexyl affin
A;Reference number: S74119; MUID:97054624; PMID:8898921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth Reference number: A31000; MUID:85076667; PMID:6510420 .A31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F.; Legrand, D.; Spik, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Species: Capra aegagrus hircus (domestic goat)
|Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
|Accession: JC2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 3-701, SWKPVN <PAN>
A;Experimental source: normal breast tissue
R;Metz-Boutrigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen,
Eur. J. Blochem. 145, 659-666, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GDB:119368; OMIM:150210
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nes 11; Conserv
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Best Local 9
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. R;Wood, D.W.; Setubal, J.C.; Kaul, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Duj C,Species: Agrobacterium tumefaciens
C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 5
A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AB2670
                                  Rjravello, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F07C3.
A;Reference number: Z2028
A;Reference number: Z2028
A;Recession: T28820
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-932 <FAV>
A;Residues: 1-932 <FAV>
A;Residues: EMBL:U50308; FIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.6%; Score 40; DB 2; Length 932; Best Local Similarity 63.6%; Pred. No. 25; Matches 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 2; Length 206;
Pred. No. 9;
2; Mismatches 4; Indels
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A,Map position: circular chromosome
C,Superfamily: pyridoxamine-phosphate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   579 FOWORSARLVK 589
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A,Molecule type: DNA
A,Residues: 1-206 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: CESP:F07C3.1
C; Accession: T28820
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                                                                                                                                          ynein beta heavy chain - Chlamydomonas reinhardtii

'Species: Chlamydomonas reinhardtii

'Jate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001

'Mitchell, D.R., Brown, K.S.

'Cell Sci. 107, 635-644, 1994

'Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.

'Reference number: 216302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Map position: IX
/Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
/Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1115/3;
/Supartamily: 426/3
/Supartamily: 426/3
/Keywords: nucleotide binding; P-loop
/1919-1926/Region: nucleotide-binding motif A (P-loop)
/2202-2209/Region: nucleotide-binding motif A (P-loop)
/2530-2537/Region: nucleotide-binding motif A (P-loop)
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Molecule type: DNA
Redidues: 1-275 < MLL.
Gross-references: EMBL-Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
Experimental source: clone F53H4
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;Species: Caenorhabditis elegans
;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Status: translated from GB/EMBL/DDBJ;
Molecule type: DNA
;Mosidues: 1-4568 MIT-
;Gross-references: EMBL:U02963; NID:9409965; PIDN:AAA19956.1; PID:9514215
;Experimental source: strain 21gr
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;Introns: 67/1; 153/1
;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.2%; Score 43; DB 2; Length 4568; 50.0%; Pred. No. 32; arive 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Roserreferences: EMBL:AC002391, NID:g2642427; PID:g2642441
A,Experimental source: cultivar Columbia
A,Experimental so
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A;Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642444
A;Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642444
A;Experimental source: cultivar Columbia
R;Lin, X; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
K.; Xoo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable cytochrome P450 At2g23220 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thallana (mouse-ear crees)
Cjapecies: Arabidopsis thallana (mouse-ear crees)
Cjate: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
Cjacession: T00510; A84622
RjRounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, November 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
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A;Introns: 182/3; 310/3
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F:312-471/Domain: cytochrome P450 homology <P45>
F:349/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A, Cross-references: GB: AE002093; NID: g2642441; PIDN: AAB87109.1;
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Length 289
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Pred. No. 33;
1; Mismatches
     ..
..
Score 38; DB 2
Pred. No. 19;
1; Mismatches
DB :
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A;Molecule type: DNA
     57.6%;
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ilarity 83.3%;
Conservative
Query Match
Best Local Similarity 50.0
Matches 6; Conservative
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R. Theologis, A.; Bcker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.Zzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G; Frager, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Asalzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G; Frager, C.M.; Venter, J.C.; Davis, R.W.
A;Accession: 86403
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Proc. Mil. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable pyridoxamine-phosphate oxidase (BC 1.4.3.5) [imported] - Brucella melitensis (q
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A;Molecule type: DNA
A;Residues: 1.-208 «KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52698.1; PID:g17983525; GSPDB:GN00190
A;Experimental source: strain 16M
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A;Cross-references: GB:AE008688; PIDN:AAL41776.1; PID:g1739129; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
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Pred. No. 9;
2; Mismatches
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C,Superfamily: pyridoxamine-phosphate oxidase
C,Keywords: oxidoreductase
                                                                                                                                                      A)Gene: pdxH
A,Map position: circular chromosome
C,Superfamily: pyridoxamine-phosphate oxidase
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Best Local Similarity 50.0
Matches 6; Conservative
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A,Map position:
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Superfamily: phytochrome; phytochrome homology
Superfamily: chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regulat
Keyword: chromoprotein; dimer; photoseptor; phytochrome homology <PHY>
(55-581/Domain: phytochrome homology <PHY>
(278) (covalent) #status predicted
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                                                 Fitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana Reference number: A84420; MUID:20083487; PMID:10617197
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Residues: 1-543 <STO>
Cross-references: GB:AE002093; NID:g2642444; PIDN:AAB87112.1; GSPDB:GN00139
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Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
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1.Introns: 211/3; 339/3

1.Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

1.Superfamily: human cytochrome P450 cytochrome P450 homology

1.341-500/Domain: cytochrome P450 homology <P45>

1.478/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Pred. No. 69;
4; Mismatches 3; Indels
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Wolecule type: mRNA
Residues: 1-1135 <4Hz
Cross-references: EMBL:U56731; NID:g1800218; PID:g1800219
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Best Local Similarity 36.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: T20D16.18; At2g23190
761-768, 1999
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A; Residues: 1-85 < PAR>
A; Cross-references: GB: AL513382; PIDN: CAD07537.1; PID: g16503529; GSPDB: GN00176 C; Genetics: A; Genetics: Best Local Similarity 60.0%; Pred: No. 8.9; Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0; Qy 1 CFQWQRXMRR 10

Qy 1 CFQWQRXMRR 10

Db 74 CDEWQRLTRK 83

Search completed: February 21, 2003, 08:02:44
JOB time: 10.6047 secs
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escherichia sus scrofa pinus sylve

chlamydia

ascaris suu escherichia

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Qute7 schizosacch
P5046 escherichia
P14632 sus scherichia
Q41046 pinus sylve
Q24325 drosophila
Q24595 drosophila
P13368 drosophila
P1368 drosophila
P1368 drosophila
P1063 escherichia
Q06399 salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tho Y.Y.;
Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
                                                                                                                                                                                                                                                                                                    27-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Contains: Lactoferroxin A;
Lactoferroxin B; Lactoferroxin C]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Mammary gland;
MEDLINE=90394839; PubMed=2402455;
Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Frimates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Mammary gland;
Liang O., Jimener-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Bone marrow, Wei X., Han J., Rado T.A., "Human neutrophil lactoferrin coding and 5' flanking region DNA
                                                                                                                                                                                                                                                                 TRFL HUMAN STANDARD; PRT; 711 AA.
P0278B; Q16780; Q16785; Q16789; O00756; Q9H1Z3; Q96KZ4;
 Q9pjj9
P44693
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Cheng H., Chen X., Huan L.;
"CDNA cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences.";
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[8]
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SYH CHLMU
YEBA HAEIN
MSSI SCHPO
AER ECOLI
TRFL PIG
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12D2 DROME
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7LES DROME
NULM ASCSU
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C
 TISSUE=Mammary gland;
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Conneely O.M.,
Submitted (MAY-1992)
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09xx18 drosophila
P93528 sorghum bic
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P41187 liberibacte
P49771 homo sapien
P12342 bost taurus
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                                                                                             ; Search time 5.2093 Seconds (without alignments) 95.544 Million cell updates/sec
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Q91t02
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P49725 D
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P20806 Q
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(c) 1993 - 2003 Compugen Ltd.
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TRFL_CAPHI
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Y008 HUMAN
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3-711 FROM N.A.

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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greo T., Tuochman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Blaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L., to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
                                                                                                                                                                                                                                                                                                                                                          "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains."; Biochim. Biophys. Acta 670:243-254 (1981).
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PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE=82046817; PubMed=6794640; Jolles J., Spik G., Montreuil J.,
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 609-711.
MEDLINE-82262043; PubMed-7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
Baker E.W.;
"Mutagenesis of the histidine ligand in human lactoferrin: iron
biding properties and crystal structure of the histidine-
253-->methionine mutant.";
Biochemistry 36:341-346(1997).
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SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031, PubMed=3477300,
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoies1s.";
                                                                                                         SEQUENCE OF 20-711.
SEQUENCE OF 20-711.
Meta-Boutique M.-H., Jolles J., Mazurier J., Schoentgen F., Legrand D., Spik G., Montreuil J., Jolles P.; "Human lactotransferrin: amino acid sequence and structural
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Haridas M., Anderson B.F., Baker B.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
resolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jolles P.; "An 88 amino acid long C-terminal sequence of human
                TISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
Powell M.J., Ogden J.E.;
"Nuclectide sequence of human lactoferrin cDNA.";
Nucleic Acids Res. 18:4013-4013(1990).
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MEDLINE=99190892; Pubmed=10089347;
                                                                                                                                                                                                                            comparisons with other transferrins."
Eur. J. Biochem. 145:659-666(1984).
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FBBS Lett. 142:107-110(1982).
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                                                                                                                                                                                                                      MEDLINE=91166929; PubMed=1369293;
Tani F., Ito K., Chiba H., Yoshikawa M.,
"Isolation and characterization of opioid antagonist peptides derived from human lactoferrin.";
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                      Jameson G.B., Anderson B.F., Noris G.E., Thomas D.H., Baker E.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                             -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                        X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
                                                                                                                                                                                        Agric. Biol. Chem. 54:1803-1810(1990)
                                  Acta Crystallogr. D 55:403-407(1999)
                                                                                                                                   CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Secreted.
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M18642; AAA86665.1; ...
AF332168; AAG4873.1; ...
BC015822; AAH15622.1; ...
BC015823; AAH15823.1; ...
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EMBL, U07643; AAB60324.1; -.
EMBL, M93150; AAB36159.1; -.
EMBL, M83202; AAB59511.1; -.
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AAB57795.1;
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31-OCT-93.
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TISSUE ADMINISTY GLAND, AND THE TESTINE ASSESSMENT OF THE TESTINE ASSESSMENT OF THE TESTINE ASSESSMENT OF THE TESTINE ASSESSMENT OF THE GOAT LACEOFERIN CO.NA. ASSIGNMENT OF THE PERVANT LOCUS to bovine UI2 Synteny group.";

Biochem. Biophys. Res. Commun. 203:1334-1332 (1994).

-i- FUNCTION: TRANSPERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BIOCREBOMATE.

-i- SUBGNIT: MONOYER (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Secreted.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
NCBL_TaxID=9925;
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Pred. No. 0.025;
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G -> A (IN REF. 2).
G -> P (IN REF. 2).
LLS -> PLF (IN REF. 2).
L -> F (IN REF. 2).
A -> P (IN REF. 2).
A -> Q (IN REF. 2).
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                      IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 2 (BY SIMILARITY)
IRON 6 (BY SIMILARITY)
ANION (BY SIMILARITY)
N-LINKED (GLCNAC. )
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                                                                                                                                       SIMILARITY. SIMILARITY. SIMILARITY.
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Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (UNI-1995) to the EmbL/GenBank/Dibb databases.
--- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
--- SUBUNIT: MONOMER (BY SIMILARITY).
--- SUBUNIT: MONOMER (BY SIMILARITY).
--- SUBCILILLAR LOCATION: Secreted.
--- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
--- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Camelus dromedarius (Dromedary) (Arabian camel).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Tylopoda; Cameludae; Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Somali; TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ131674; CAB53387.1; -.
BNBL; AF165879; AAF82241.1; -.
HSSP; O77811; IBIX.
InterPro; IRRO01156; Transferrin.
PFINITS; PRO0422; TRANSFERRIN.
SMART; SM00049; TR FER, 2.
PROSITE; PS00206; TRANSFERRIN.
PROSITE; PS00206; TRANSFERRIN.
PROSITE; PS00206; TRANSFERRIN.
PROSITE; PS00206; TRANSFERRIN.3; 2.
PROSITE; PS00207; TRANSFERRIN.3; 2.
PROSITE; PS00207; TRANSFERRIN.3; 2.
                                                                    0;
                      Length 711;
                                                                  1; Indels
                    Score 64; DB 1; I
Pred. No. 0.00024;
0; Mismatches 1;
                                                                                                                                                                                                                                                    TRFL CAMDR STANDARD; PRT; 708 AA. O9TUM0; Q9MZSS; 16-CT-2001 (Rel. 40, Last sequence update) 16-CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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Best Local Similarity 91.7
Matches 11; Conservative
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rissum=uterus;
                            RESULT 4
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                               EMBL, U53877, AAA97958.1; --
EMBL, X78922, CAA55517.1; --
HSSP, O77699; ICE2.
III CAA55517.1; --
HSSP, O77699; ICE2.
III CAA55517.1; --
PFam, PF004156; Transferrin, 2.
PRINITS, PR00422, TRANSFERRIN.
SMART; SM00049; TRANSFERRIN.
SMART; SM00049; TRANSFERRIN.
PROSITE; PS00206; TRANSFERRIN.2; 2.
PROSITE; PS00206; TRANSFERRIN.3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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C -> R (IN REF. 2).
C -> R (IN REF. 2).
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F -> R (IN REF. 2).
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IRON 2 (BY SIMILARITY).
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N-LINKED (GLCNAC...)
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN.
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Liu Y., Teng C.T.;

Liu Z., Teng C.T.;

J. Biol. Chem. 266:21880-21885(1991).

J. Biol. Chem. 266:21880-21885(1991).

- FONTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

- FONTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.

- SUBUNIT: MONOWER:

- SUBUNIT: MONOWER:

- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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REMBL; D88510; BAA13633.1; -...

REMBL; M74778; AAA39427.1; -...

REMBL; RE
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                Pentecost B.T., Teng C.T.,
"Lactorransferrin is the major estrogen inducible protein of
uterine secretions,";
U. Biol. Chem. 262:10134-10139(1987).
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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LACTOTRANSFERRIN.
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TREL MOUSE STANDARD; PRT; 707 AA. 198071, P70690; Q61799; Q922P2; Created) 1-4UG-1988 (Rel. 08, Created) 1-4UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
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-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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J. cell Sci. 107:635-644(1994).
J. cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF BUKARYOTIC CILIA AND FLAGELIA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
DYNEIN HAS ATTAKE ACTIVITY.
-!- SUBBUXIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                       ANION (POTENTIAL).
ANION (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MR -> IQG (IN REF. 1).
R -> Q (IN REF. 2).
M -> L (IN REF. 2).
S -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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M -> L (IN REF. 2).

A -> D (IN REF. 2).

A -> D (IN REF. 1).

E -> G (IN REF. 1).

L -> V (IN REF. 1).

L -> V (IN REF. 1).
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01-NOV-1997 (Rel. 35, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 4568 AA.
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MEDLINE=94274778; PubMed=8006077;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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544
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707 AA;
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-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
-!- SUBGNIT: MONOMER.
-!- SUBCRILIAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
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MICROTUBLIE BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
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Pfam; PF03028; Dynain heavy; 1.

Motor protein; Microtubules; Dynain; ATP-binding; Flagella; Coiled coil.

Coiled coil.

COLLED COIL (POTENTIAL)

DOMAIN 1158 1175 COILED COIL (POTENTIAL)
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Pred. No. 11;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 ATP (POTENTIAL).
86 ATP (POTENTIAL).
519961 MW; 9A9AS393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"cDNa sequence of mare lactoferrin.";
submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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15-UUL-1999 (Rel. 38, Last sequence update)
15-UUN-2002 (Rel. 41, Last amnotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment)
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Last sequence update) Last annotation update)

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Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Perryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                    SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                       ubmitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
30-MAY-2000 (Rel. 39,
16-OCT-2001 (Rel. 40,
                                                                                                                                        SEQUENCE FROM N.A.
                  Nebula protein.
NLA OR CG6072.
                                                                                                                Eemales
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                                                                                                                                                                     (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
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Pred. No. 9.3;
3; Migmatches 2; Indels
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IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                            LACTOTRANSFERRIN.
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N-LINKED
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                                                                                    PDB, 1BTV, 02-DEC-98.
PDB, 1BTV, 02-DEC-98.
PDB, 1BTV, 02-PEB-99.
PDB, 1BTV, 02-PEB-99.
INTER-PRO, IPRO01156; Transferrin.
Pfam; PPO0405; transferrin; 2.
PRINTS; SMO0094; TR FER; 2.
PROSITE; PSO0205; TRANSFERRIN 1; 2.
PROSITE; PSO0205; TRANSFERRIN 1; 2.
PROSITE; PSO0206; TRANSFERRIN 1; 2.
PROSITE; PSO0206; TRANSFERRIN 2; 2.
                                                                             EMBL; AJ010930; CAA09407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75991 MW;
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Conservative
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Best Local Similarity
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BINDING
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Matches
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STRAINBERKELP, NAME OF THE R.A., EVARR C.A., GOCCAPIR J.D.,
AGAMEN MEDINESCREEF S.E., Holf R.A., EVARR C.A., GOCCAPIR J.D.,
AGAMEN MEDINESCREEF S.E., Holf R.A., EVARR C.A., GOCCAPIR S.N.,
AGAMEN MEDINESCREEF S.E., Holf R.A., EVARR C.A., GOCCAPIR S.N.,
AGAMEN MEDINESCREEF S.E., Holf R.A., SARBULTRER R.A., Henderson S.N.,
SULTON G.G., WOTTHMEN J.R., ENGLAIDS S., ASHBULTRER R.A., MALLOS G.L.G.,
AMARIEL M.C., ROSCREEF Y.H.C., Blazej R.G., Champe M., Pefeiffer B.D.,
AMARIEL M.C., ROSCREEF R.G., Helf G., NARION C.R., MIKIOS G.L.G.,
AMARIEL M. M., Beau A., Barandale M., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Calver B. Bouck J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Calver B. Bouck J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Calver B. Bouck J., Bayraktaroglu L., Beasley E.M.,
Burris K.C., Bousm D.A., Butler H., Cadieu E., Center A. Chandra I.,
Burris K.C., Bousm D.A., Butler H., Cadieu E., Center A., Chandra I.,
Burris K.C., Bouchan M.R., Bonck J., Brandari D., Bertier S.,
Bockova D., Calver B., Downes M., Dugan R.Coh S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferrace S., Fleischmann W.,
R.A., Gong F., Gorrell J.H., Gu Z., Gunar P., Harris M.,
Alali M., Kaludh F., Karpen G.H., Wei M.-H., Ibegam C.,
Jalali M., Kaludh F., Karpen G.H., Wei M.-H., Ibegam C.,
Jalali M., Mattel B.E., Kodieu C.D., Kraft C., Wernison J.A., Norley M.,
Bakkulovo G., Milshina N.V., Mobarry C., Morris G., Monne S., Black M.G.,
R. Beinert K., Remington K., Nimpson K., Nimzry D.M., Nalson D.L,
R. Balazolo M., Pitthan G.S., Pan S., Pollock M. P., Fank M. R.,
R. Balazolo M., Pitthan G.S., Pan S., Pollock M., Stude S., Pan S.,
R. Balazolo M., Pitthan G.S., Pan S., Pollock M., Stude S., Pan S.,
R. Shieb B.C., Stden K.A., Nimpson M., Stude S., Yan S., Yan R.,
R. Mang Z.-Y., Wassarman D.A., Weinserok G.M., Waissenbach J.,
R. Walliams S.M., Woodage T., Worley K.C., Wu D., Yan R., Sprack M., Weinserolo M., Streke E., Spradling A.C., Stan M., Weinser B., Sprack M., Weinser B., Sprack M., Weinser B., Sprack M., Weins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; AE003712; AAF55285.1; -.
SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
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Gaps

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292 AA.

PRT;

NLA DROME STANDARD; Q9XZL8; Q9V391; 30-MAY-2000 (Rel. 39, Created)

PAU

RESULT 7
NLA DROME

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                                               ö
                                                                                                                                                                                                                                                                                                                                      Sorghum bicolor (Sorghum) (Sorghum vulgare).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THAT ABSORBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLANCE DESCRIPTION OF THE REPORTED REPORTED FOR THE PROPERTY OF THE PROPERTY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PRR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PRR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE RECONDING THE SMALL SUBDINT OF RELIGIORS BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTABLE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENES () IN A NEGATIVE FEEDBACK FASHION (BY
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBDITT: HOMODINER (BY SIMILARITY).
-1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-1- SIMILARITY: BELONGS TO THE PHYTOCHRONE FAMILY.
-1- SIMILARITY: CONTAINS 2 PAS (PEE-ARNT-SIM) DIMERIZATION DOMAINS.
-1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
-1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97198856; PubMed=9046599;
Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.E.,
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                               ö
  57.6%; Score 38; DB 1; Length 292; 54.5%; Pred. No. 6; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                              1135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, U56731; AAB41399.1; -. InterPro; IPR003594; ATPbind_ATPase. InterPro; IPR003109; GAF. InterPro; IPR004599; HIS KIN sig. InterPro; IPR00561; His_kinĀ. InterPro; IPR001601; PAC. InterPro; IPR001014; PAC. InterPro; IPR001014; PAC. Gomain. InterPro; IPR001014; PAS. Gomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; PP00360; phytochrome; 1. Pfam; PP00310; signal; 1. Pfam; PP00510; signal; 1. Pfam; PP00599; PAS; 2. Pfam; PP01590; GAF; 1. Pfam; PP015133; PHATPASS C; 1. PRINTS; PR01033; PHATPASS C; 1. PRINTS; PR01033; PHATPASS C; 1.
Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                         150 FOWLRSFRRLR 160
                                                                                  2 FOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Phytochrome C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=IT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latrellle P.,
COUTTING L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; HisKA; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAC; 1.
SMART; SM00091; PAC; 1.
SMART; SM00091; PAC; 1.
FAC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roland K.L., Esther C.R., Spitznagel J.K.,
"Isolation and characterization of a gene, purD, from Salmonella typhimurium that confers resistance to polymyxin when expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 1135;
Pred. No. 23;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                           748 822 PAS 2.
902 1122 HISTIDINE KINASE.
321 321 CHROWDHORE (BY SIMILARITY).
1135 AA, 126315 MW, AFCC934B7592DB4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 AA
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymyxin B resistance protein pmrD.
PMRD OR STM2304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple copies.";
J. Bacteriol. 176:3589-3597(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94266712; PubMed=8206837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    775 CLEWNKAMOKI 785
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BINDING
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Planet P., Jagoueix S., Bove J.M., Garnier M., "Detection and characterization of the African Citrus Greening Liberobacter by amplification, cloning and sequencing of the rplKAJL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, I BETA CHAIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate \{RNA\} (N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BETA' CHAIN.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           group
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                                                                                                                                                                                                                                                                                                                                                                                      Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
                                                                          Score 37; DB 1; Length 85; Pred, No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
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Pfam; PF00562; RNA pol B; 1.
PROSITE; PS01166; RNA POL BITA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16731 MW; 815D6EDD66FD8943 CRC64;
          Stydene, SG10304, pmrD.
Antibiotic resistance, Complete proteome.
SEQUENCE 85 AA; 9749 MW; 1B1922419EA50CCA CRC64;
                                                                                                                                                                                                                                                           146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                           1; Mismatches
EMBL; AE008803; AAL21205.1; -.
                                                                            56.1%;
60.0%;
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                                                                              Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6, Conservative
                                                                                                                                                                                                                                                         STANDARD;
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SEQUENCE 146 AA;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                              CFOWORXMRK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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ID RPOB_LIBAF
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1 CFQWQRXMRK 10

CVÓWSRGARK 19

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RESULT 11 FL3L\_HUMAN

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-!- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here)
and 2/soluble; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20343011; PubMed=10881197;
Savvides S.W., Boone T., Karplus P.A.;
Savvides S.W., Boone T., Karplus P.A.;
"It13 ligand structure and unexpected commonalities of helical
bundles and cystine knots.";
Nat. Struct. Biol. 7:486-491 (2000)
-1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004213; Flt3_lig.
Pfam; PF02947; flt3_lig; 1.
Stokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;
3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of human and murine flt3 ligand genomic loci."; Oncogene 11:1165-1172(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94225842; PubMed=8180375;
Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,
Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.;
"Cloning of the human homologue of the murine flt3 ligand: a growth
factor for early hematopoletic progenitor cells.";
Blood 83:2795-2801(1994).
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
15 cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3
FLT3LG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91195422; PubMed=8145851;
Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
Hannum C., Culpepper J., Hudak S.,
Bazan J.F., Kaefeelin R., Hudak S., Wagner J., Mattson J., Luh J.,
Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G.,
Zlornik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
higand for FIT3/FLK2 receptor tyrosine kinase regulates growth of
haematopoletic stem cells and is encoded by variant RNAs.";
Nature 368:643-648(1994).
                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FACTORS AND INTERLEUKINS.
-!- SUBUNIT: Homodimer (isoform 2).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=96032581; PubMed=7566977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U04806; AAA17999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U03858; AAA19825.1; -. U29874; AAA90949.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
DSSTLPPPWSPRFLEATA -> VETVFHRVSQDGLDLITS
(IN ISOFORM 2).
G -> A (IN REF. 1).
73B95BF693B4CECF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88212503; PubMed=2835311;
Meinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
Reeves R., Magnuson J.A.;
"Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
Immunology 63:603-610(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2010 (Rel. 140, Last annotation update)
Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PS5) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Swkaryota, Metazos, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae: Bos
                                                                                                                                           (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                 Score 36; DB 1; Length 235;
Pred, No. 11;
                                                                                                                                                                                                                                                                                                                  4; Indels
                SL CYTOKINE.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                    1; Mismatches
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N-LINKED
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                                                                                                                                                                                                                                                                               54.5%;
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                                                                                                                                                                                                                                              26416
                                                                                                                                                                                                                                                                                                                    5; Conservative
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235 AA;
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                                                                                                                                                                                                                                                                                                  Local Similarity
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P12342;
                                 DOMAIN
TRANSMEM
                                                                  DOMAIN
DISULFID
DISULFID
DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-RB-1996 (Rel. 33, Last anottation update)
Interlebkin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PSS) (TAC antigen) (CD2S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                         BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                        ö
                                                          Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
SIGNAL
                                                                                                                                                                                                                                            Score 36; DB 1; Length 275;
Pred. No. 13;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Verhagen A.A.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                      4901BBF9A4862390 CRC64;
                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                            275 AA
                                                                                                                                        SUSHI 2.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                         POTENTIAL
PIR; S07442; S07442.
HSSP; P01589; 11LM.
INTERPRO; IPR000436; Sushi_SCR_CCP.
Pfam; PP00084; sushi; 2.
SWART; SM00032; CCP; 2.
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                                                                                                                                                                                                                                                54.5%;
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                                                                                 22443
22643
2262
2752
2752
1858
1968
1099
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263
263
1223
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1233
1952
1090
1090
1090
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                           DOMAIN
TRANSMEM
DOMAIN
                                                                                                                              DOMAIN
DOMAIN
DISULFID
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                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                          SEQUENCE
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                                                                                CHAIN
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IL2A_SHEEP
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BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
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AC 29LT02;
DT 16-OCT-2001
DT 16-OCT-2001
DF POTENTIAL CA
GN AT5G23630 OR
OS ARABIGOSES
OC EUKARYOCEA; V
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ARE REVERGELY INTERCONVERTIBLE BY LIGHT: THE RF CARM THAT ABSORBS

ARE REVERGELLY INTERCONVERTIBLE BY LIGHT: THE RF CARM THAT ABSORBS

MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT

ABSORBS MAXIMALLY IN THE PAR RED REGION. PHOTOCONVERSION OF PR IN

PER INDUCES AN ARRAY OF MORPHOGENIC RESPONES, WHEREAS

RECONVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE

RESPONSES. PPR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR

GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Nipponbare;
STRAIN=cv. Nipponbare;
Tahlir M., Kanegae H., Takano M.;
Phytochrome C (PHYC) gene in rice: isolation and characterization of
a complete coding sequence.";
(In) Plant Gene Register PGR98-210.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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SEQUENCE OF 275-378 FROM N.A.
MEDLINE=97019052; PubMed=8855668;
Mathaws S., Sharrock R.A.;
Mathews S., Sharrock R.A.;
"The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                           1; Receptor; Repeat; Signal; Sushi.
BY SIMIDALITY.
INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
SUSHI 1.
SUSHI 1.
                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N.LINYED (GLCHAC. . .) (FOTENTIAL).
S. -> T (IN REF. 2).
W, 1101A2DB5ACSA088 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                   54.5%; Score 36; DB 1; Length 275; 50.0%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHYC_ORYSA STANDARD; PRT; 1137 AA. Q9ZWT9; P99429; 16-OCT-2001 (Rel. 40, Last sequence update) 15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                        PIR; S18910; S18910.
PIR; S1899; S18899.
PIR; JC1113; JC1113; JC1113; JC1113; JC1113.
HSSP; PO1589; ILIM.
InterPro; IPRO00494; Sushi_SCR_CCP.
PEam; PPO0084; sushi, 2.
SMART; SM00032; CCP; 2.
                                                                                                                                                                                                                                                                                                                                                                          30904 MW;
                                                                                                                                                              Transmembrane, Glycoprotein;
               EMBL; Z11560; CAA77652.1; -. EMBL; X60149; CAA42723.1; -. EMBL; A19167; CAA01447.1; -.
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152 1
80
166 1
275 AA;
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nes 6, Conserv
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TRANSMEM
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DOMAIN
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CONFLICT
SEQUENCE
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DISULFID
DISULFID
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PHYC_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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PROTOCHLOROPHYLLIDE REDUCTAGE, RRNA, ETC. IT ALSO CONTROLS
THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK PASHION.
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                -:- PTM: CONTAINS ONE COVALENTY LINKED TETRAPYRROLE CHROMOPHORE.
-:- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
-:- SIMILARITY: CONTAINS 2 PSA (PERFARMY-EAM) DIMERIZATION DOMAINS.
-:- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
-:- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TICRFAMS, TICR00229; sensory_box; 2.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS00245; PHYTOCHROWE 1; 1.
PROSITE; PS50046; PHYTOCHROWE 2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-0cr-2001 (Rel. 40, Created)
16-0cr-2001 (Rel. 40, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
Potential cation-transporting ATPase (EC 3.6.3.-).
Arg523280 OR MQMI.1.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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Pred. No. 54;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOPHORE (BY SIMILARITY)
F -> S (IN REF. 2).
C -> S (IN REF. 2).
WW; F2A520181CFB7B32 CRC64;
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PAS 2.
HISTIDINE KINASE.
CHROMOPHORE (BY S)
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Interpro; IPR003018; GAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003151 HGS KIN Sig.
InterPro; IPR003661; His_Kin Sig.
InterPro; IPR003661; His_Kin Sig.
InterPro; IPR001610; PAG.
InterPro; IPR001610; PAG.
InterPro; IPR001294; Phytochrome.
Pfam; PR00360; phytochrome; 1.
Pfam; PR00360; phytochrome; 1.
Pfam; PR00361; signal; 1.
Pfam; PR01590; GAF; 1.
Pfam; PR015818; HATPase c; 1.
PRINTS; PR01033; PHYTOCHROME.
SWART; SM00387; HATPase c; 1.
SWART; SM00387; HATPase c; 1.
SWART; SM00388; HATPASE c; 1.
SWART; SM00388; HATPASE c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3MBL; AB018442; BAA74448:1; -.
3MBL; U61207; AAB41996:1; -.
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279 27
292 29
1137 AA;
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777 CLEWNEAMOKI 787
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                                                                                                                                                                                                                                       'Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence ceatures of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00119; CATATPASE.
PROSITE; PS00154; ATPASE E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                            SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Saro S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                        Clones.";

DNA Res. 7:31-63(2000).

-!- PUNCTION: INVOLVED IN TRANSPORT OF CATIONS (POTENTIAL).

-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY

(E1-E2 ATPASES). SUBFAMILY V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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Pred. No. 56;
3; Mismatches 2; Indels
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB025633; BAA97238.1; -.
InterPro; IPR001454; ATPase B1-E2.
InterPro; IPR001454; Hignase/hydriase.
Pfan; PF00122; B1-E2 ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
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1179 AA; 131115 MW;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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TRANSMEM
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SEQUENCE
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Gaps

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1144 CYSWERLLR 1152
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Search completed: February 21, 2003, 07:51:37 Job time : 6.2093 secs

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29ygc0 human immun
09ygc0 human immun
09ygc0 human immun
09ygc0 human immun
09yij7 human immun
09yij7 human immun
09yij2 human immun
09yij2 human immun
09yij2 human immun
09yij3 aranobacteri
09nav0 homo sapien
09nav0 homo sapien
09nav0 homo sapien
09nav0 homo sapien
09nav3 homo sapien
09sessa encephalito
08sessa encephalito
08sessa encephalito
08sessa encephalito
08sessa encephalito
08sessa encephalito
08sessa encephalito
                                                                                                                     O9sws6 lycopersico
O8z536 salmonella
                                                         022185 arabidopsis
022188 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 'Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human) (Fragment).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.4%; Score 59; DB 4; Length 711; 90.9%; Pred. No. 0.0067; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBTCD2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Lactotransferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                              099C6N2
022185
022185
095W56
095W56
09YQC1
09YQC1
09YQ17
09YJ17
0
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Q9ZTP0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         094937
062582
QBSRG3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBSQI6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
10
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      Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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Q9UCYS
ID Q9UCY
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Q8TCD2
   8 6
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Q9tcd2 homo sapien
Q9tr80 ovtza saties
Q9xt86 ovtza satie
Q9xtB5 ovtza satiu
Q9x780 caenorhabdi
Q19153 caenorhabdi
Q1986a0 rhizobium 1
Q8uc2 agrobacteri
Q9xr88 rhizobium m
Q8xe2 ralsconia s
Q8xe2 ralsconia s
Q8xez homo sapien
Q97855 human immun
Q77855 human immun
                                                                                                                                                                                                                                                  (without alignments)
114.078 Million cell updates/sec
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                                                                                                                                                                                                                   February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   671580
                              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671580 segs, 206047115 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                       OM protein - protein search, using sw model
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Q9UCY5
Q9UCY5
Q9XFD5
Q9XFD1
Q93780
Q19153
Q9BCAC
Q92RH3
Q8XFK3
Q8XFK3
Q8XFK3
Q8XFK3
Q8YFK3
Q8YFFK3
Q8YFF
Q
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Gapop 10.0 , Gapext 0.5
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1: sp archea:*

3: sp bacteria:*

4: sp fungi:*

4: sp human:*

5: sp human:*

6: sp mamman:*

7: sp_mhc:*
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sp_phage:*
sp_phant:*
sp_rodent:*
sp_virus:*
sp_virus:*
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sp_bacteriap:*
sp_archeap:*
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faximum DB seq length: 200000000
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66
1 CFGWQRXMRKVR 12
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Query
Match Length DB
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Perfect score:
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Gaps

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Eukaryora; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
Storage proteins in sessue...;
J. Agric. Food Chem. 47.4932-4938 (1999).

BERL, Agric. Prod Chem. 47.4932-4938 (1999).

Interpro; IPR001631; AAI.

Interpro; IPR00168; Try/amyl inther.

Pfam; PR00234; tryp_alpha_amyl; 1.

PRINTS; PR00499; AAI; 1.

SEQUENCE 188001499; AAI; 1.

SEQUENCE 148 AA; 1.7524 MW; BA46B033BA13E3DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Caenorhabditis elegans.
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CFQWERLGKK 70
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Q93780;
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Matches
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11D 099
14C 099
15C 099
16C 099
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Cytochrome P450 (Fragment).
Cytochrome P450 (Fragment).
Enkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae,
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                     Sato I., "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A.
TISSUB=PANICLE,
Liu J., Yang J.,
"Suppression subtractive hybridization (SSH) identified candidate
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0
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             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                             83.3%; Score 55; DB 4; Length 38; 90.9%; Pred. No. 0.0019; Live 0; Mismatches 1; Indels
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MEDIINE=55127729; PubMed=7827104;

MEDIINE=55127729; PubMed=7827104;

Biochim. Biophys. Acta 1243:25-32 (1995).

HSSP: 077698; ICE2.

HTGSPPO; IPRO01156; Transferrin.

Pfam; PG00405; transferrin; 1.

SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                             InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5BBDDBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 AA.
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                                                                                                                                                                                        seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995)
HSSP; P02788; 1BKA.
                                                                                     SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FOWORXMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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                SORTERFERENCE
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MEDLINE=20074970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
"Molecular cloning of 115 globulin and 28 albumin, the two major seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Sesamum indicum (Oriental sesame) (Gingelly).
Wakaryota, Viridiplantae, Streptophyta, Babryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotylddons, core eudicots;
Asteridae, euasferids I; Lamiales, Pedaliaceae, Sesamum.
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th Similarity 60.0%; Pred. No. 2.3; 6; Conservative 2; Mismatches 2; Indels
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PRT;

PRELIMINARY;

none;

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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=2160856; PubMed=11743193; MeDLINE=2160856; PubMed=11743193; Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Chara V.K., Zhou Y., Chen Y., Ranb E.D., Bovee D. Sr., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendening J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
MCBI _TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyridoxamine 5'-phosphate oxidase.

PDXH OR ATU0760 OR AGR_C 1381.

Agrobacterium tumefaciens (strain C58 / ATCC 33970).

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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BMBL, ADO03011; ABB53533.1; -.

InterPro; PR000659; Pyridox oxidase.

Pfam; PF01243; Pyridox oxidase; 1.

ProDom; PD006312; Pyridox oxidase; 1.

IGREPAMS; TICR00558; paxH; 1.

PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=WAFF303099;
MEDLINE=21082930; PubMed=11214968;
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MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                             Pyridoxamine 5'-phosphate oxidase.
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Best Local Similarity 50.0%;
Matches 6; Conservative
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QBUHC2
               DDT TO DO THE PROPERTY OF THE 
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C.elegans: A platform for investigating biology."; science 282:2012-2018(1998).
EMBL; Z31089; CAB03137.1; -. SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.6%; Score 40; DB 5; Length 275; 63.6%; Pred. No. 9.7; 1ve 1; Mismatches 3; Indels
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STRAIN-BRISTOL N2;
STRAIN-BRISTOL N2;
Uprect Submission.";
"Direct Submission.";
"Direct Guldission.";
"Direct Guldission.";
"Direct Submission.";
"Direct Su
                                                                                                            Dobson R.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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STRAIN=BRISTOL N2;
Favello A., Gattung S.;
"The sequence of C. elegans cosmid F07C3.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 105.1 KDa protein.
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STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.0-
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
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[1]
SEQUENCE FROM N.A.
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019153

Query Match

Matches

ESULT 8 986A0

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Gaps

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Indels

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SEQUENCE FROM N.A.

STRAIN=16M / ATCC 21456 / BIONTYPE 1;
STRAIN=16M / ATCC 21456 / BIONTYPE 1;
STRAIN=16M / ATCC 21456 / BIONTYPE 1;
MEDLINE=20020109; PubMed=1175668 R.J., Patra G., Mujer C., Los T.,
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
DelVecchio V.G., Rapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ablonski L., Larsen N., D. Souza M., Bernal A., Mazur M., Golteman E.,
A selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
A selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
The genome sequence of the facultative intracellular pathogen
The genome sequence of the facultative intracellular pathogen
The group sequence of the facultative intracellular pathogen
The group Register Sci. U.S.A. 99:443-448(2002).

EMBL; ABO9587; AALS2698.1; -
BRL; ABO9587; AALS2698.1; -
BRL; ABO9587; Pyridox_oxidase.
Probom; Po006312; Pyridox_oxidase.
Probom; Po006312; Pyridox_oxidase; 1.
TIGRPMA; TIGRROSS; pdxH; 1.
PROSITE; PS01064; PYRIDOX Oxidase.
Oxidoreductase; Complete Proteome.
Sp. Oxidoreductase; Complete Proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Curnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
Weissenbach J., Boucher C.A.;
Mature 415.497-502(2002)
                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid megaplasmid.
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 16; Length 208;
Pred. No. 11;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.1%; Score 39; DB 16; Length 279; 41.7%; Pred. No. 15; ive 3; Mismatches 4; Indels
        01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (BC 1.4.3.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31541 MW; ABB38818004B2EDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ICC protein homolog.
ICC OR RSP0534 OR RS00414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AL646079, CAD17685.1, ...
InterPro; IPR004843; M-ppestrase.
InterPro; IPR004844 S/T phosphtse.
Pfam; PR0049; Metallophos; 1.
Plasmid; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                    Brucella melitensis.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Q8XSE2
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Hounniel K., Gordon J., Vaudin W., Tarchouk O., Epp. A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., Ethe plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.", Science 294:332-3281(201).

EMBL, AB0090043; AAK86569.1; -.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Baistard P., Backer A., Boutry M., Cadieu B., Dreano S., Gloux S., Godzie T., Goffeau A., Kahn D., Kiss B., Lelaure V., Masuy D., Pohl T., Portetalle D., Puehler A., Purnelle B., Ramsperger U., Pohl T., Portetalle D., Puehler A., Purnelle B., Ramsperger U., Ranary Sis of the chronosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.", P8892 (2001).

EMBL, ALS91785, CAC45467.1; -

InterPro, IPR000659; Pyridox_oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 1.4.3.5).
PDXH OR R00895 OR SMC00069.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group;
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Pred. No. 11; 4; Indels
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                   59.1%; Score 39; DB 16; Length 206; ilarity 50.0%; Pred. No. 11; Conservative 2; Mismatches 4; Indels
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Oxidoreductase; Complete proteome.
SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;
                                                                                                                                                                                                                                                                                                                     206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
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ProDom, PD006312; Pyridox oxidase; 1.
TIGRFAMs; TIGR00558; pdxH; 1.
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWORXMRKVR 12
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                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 206 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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SEQUENCE FROM N.A.
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01-MAR-2002
01-MAR-2002
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Q92RH8 **Q92RH8** 

RESULT 10 **092RHB** 

Best Loca Matches

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OBYFK3

RESULT 11 QBYFK3

1 CFOWORXMRKVR 12

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Described FROM N.A.

SEQUENCE FROM N.A.

A ISSUE AT., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A ISSOE T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nadai K., Sugano S., Shiratori A., Sudo H.,

A Nishikawa T., Nadai T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

A Takahashi M., Chiba Y., Ishida S., Murakawa K., Cho Y., Takiguchi S.,

Matanabe S., Kimura K., Ishida S., Murakawa Y., Nagahari K., Masuho Y.,

A Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

A Ninomiya K., Iwayanagi T.,

"NEDO human CDNA sequencing project.";

"NEDO human CDNA sequencing project.";

SUBLI, ROSO203; BAA92048.1;

"NESP: P21707; IBTN.

R HSSP: P21707; IBTN.

R HSSP: P21707; IBTN.

R HSSP: P2109; IBTN.

R PROJES S., SAMARIS S., I.

R PROJES S., SAMARIS S., I.

R PROSITE; PS00030; RRM RNP.1; UNKNOWN I.
                                                                                                                                                                                  01--UN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ1175.
Bukaryoca, Merazoa; Chordata; Craniata; Vertebrata; Eutheroatomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. LEB TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CT-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ11175 fis, clone PLACE1007375, weakly similar to phorbol ester/diacy1glycerol binding protein UNC-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.1%; Score 39; DB 4; Length 306; 55.6%; Pred. No. 17; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=PANCREAS;
Strausberg R.;
Strausberg R.;
Strausberg A.;
Strausberg A.;
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025708; AA425708.1; -..
Hypothetical protein.
Hypothetical protein.
FOOTHOR B. 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
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                                                                                                                                                           PRELIMINARY;
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244 CFÓWEKGTRIAK 255
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MEDLINE=55191002; PubMed=7884875;
MEDLINE=55191002; PubMed=7884875;
Mulder-Kampinga G.A., Silmonon A., Kuiken C.L., Dekker J.,
Scherpbier H.J., de Perre P., Boer K., Goudsmit J.;
Scherpbier H.J., de Perre P., Boer K., Goudsmit J.;
"Similarity in env and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is unralated to time of HIV-1 RNA positivity in the child.";
J. Virol. 69:2285-2296(1995).
EMBL, 247867; CAA87881.1;
"InterPro; IPRONO777; GP120.
Pfam; PRO0516; GP120.
Pfam; PRO0516; GP120.

ALDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.6%; Score 38; DB 15; Length 91; 60.0%; Pred. No. 7.4; tive 2; Mismatches 2; Indels
     DB 4; Length 466,
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                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Last annotation update)
Query Match
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Matches 6; Conserv
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NON TER
SEQUENCE
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Q77855;
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Human lactoferrin
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| SIDS2/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDS2/gcddata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDS2/gcddata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDS2/gcddata/geneseq/geneseqp-embl/AA198.DAT:*
| SIDS2/gcddata/geneseq/geneseqp-embl/AA198.DAT:*
| SIDS2/gcddata/geneseq/geneseqp-embl/AA198.DAT:*
| SIDS2/gcddata/geneseqg/geneseqp-embl/AA198.DAT:*
| SIDS2/gcddata/geneseqg/geneseqp-embl/AA199.DAT:*
| SIDS2/gcddata/geneseqg/geneseqp-embl/AA2000.DAT:*
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| SIDS2/gcddata/geneseqg/geneseqp-embl/AA2000.DAT:*
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| SIDS2/gcddata/geneseqg/geneseqp-embl/AA2000.DAT:*
| SIDS2/gcddata/geneseqg/geneseqg-embl/AA2000.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM protein - protein search, using sw model
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AAY78038
AAY78046
AAY780804
AAY78089
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AAY78049
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Gapop 10.0 , Gapext 0.5
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	4.2	, 4,		18	15	AAR69352		Human lactoferrin
	25	9		18	17	AAW13397		Advanced glycosyla
	26	9.	٠	18	21	AAY78033		Human lactoferrin
	27	<b>4</b> , 2	•	61.	27	AAY68867		Amino acid sequenc
	0 0	1, 4 1, Q	•	20	7	AAR21810		Anti microbial pen
	010	, 4,		202	14	AAR44841		Lactoferrin-relate
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	39	4	•	20	17	AAR98553		Peptide for anti-u
	040	4, s	•	20	1,	AAR91852	-	Lactoferrin-derive
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DE:	Human l	actofe	rrin de	erived	pepti	de SEQ	ID NO:74.	
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ž	nos	I.A, Ma	Mattsby-	Baltz	ezI	, Baltzer	L, Dolphin GT	
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AAY78001 to AAY78100 represent peptides having sequences based on human
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Best Local Similarity 91...
These 11; Conservative
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29-DEC-1998;
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Dolphin GT;

Baltzer L,

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06-JUL-1998;
17-JUL-1998;
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                                                                                                                                                                             AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intestine through and through and are then transported through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food stuffs such as infant formula food. The peptides are also functioned and becerving as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used alinically on a broad basis because of high production costs. Therefore, provision of peptides because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                Claim 22; Page 35; 102pp; English.
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91.7%;
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98SE-0004614.
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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98SE-0002562.
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Best Local Similarity 91.7
Matches 11; Conservative
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12 AA;

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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad dasis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Matches 11; Conserv
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Been though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a musosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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llarity 91.7%; Pred. No. 7.9e-05;
Conservative 0; Mismatches 1; Indels
Score 64, DB 21, Length 12;
Pred. No. 7.9e-05;
0, Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                   AAY78086 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
                                      llarity 91.7%;
Conservative
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Best Local Similarity
Matches 11, Conserv
                                         Similarity
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Best Local Simil
Matches 11; C
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29-DEC-1998;
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ID AAXY

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Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Human lactoferrin derived peptide SEQ ID NO:90.

(first entry)

25-APR-2000

AAY78090;

AAY78090 standard; Peptide; 12 AA.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as univary tract infections, orlitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Broan though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used as used as because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                    Human, lactoferrin, modification, infection, inflammation, tumour;
food, infant formula, anti-inflammatory, anti-microbial, anti-tumour;
urinary tract infection, colitis, Candida infection, fungicidal;
bactericidal, preservative.
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                                                                                                                    AAY78089 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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                             1 CFÓWÓREMRKVR 12
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CFOWORXMRKVR
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                   AAY78089;
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Dolphin GT;

Baltzer L,

Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB.

98SE-0002441. 98SE-0002562. 98SE-0004614.

06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

99WO-SE01230,

06-JUL-1999;

13-JAN-2000

WO200001730-A1.

Homo sapiens

Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as urinary tract infeations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 37; 102pp; English
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es 12; Conserv
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AAY78037
ID AAY71
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AC AAY71
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Gaps ô

Score 64; DB 21; Length 12; Pred. No. 7.9e-05; 0; Mismatches 0; Indels

97.0%; sc.\_ 100.0%; Pred

Query Match Best Local Similarity 100. Matches 12; Conservative

12 AA;

Sequence

CFQWQRXMRKVR 12 CFÓWORXMRKVR 12

RESULT 7

Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary trace infections, collitis, and candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colltis; Candida infection; fungicidal;
bactericidal; preservative
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colltis; Candida infection; fungicidal;
bactericidal; preservative.
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Pred. No. 8.6e-05;
0; Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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11; Conservative
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Matches
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Dolphin GT;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as unimary tract infections and/or tumours. The peptides can also be used membrane), inflammations and/or tumours. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides they cannot be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 8.6e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                       Dolphin GT
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                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 74; 102pp; English.
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91.7%;
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Best Local Similarity 91.7
Matches 11, Conservative
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                                  WO200001730-A1
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                                                                                                06-JUL-1999;
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                                                                                                                                                                                                                                       Hanson LA,
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AAY78049
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Beyen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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                                                                                                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB 21; Length 13; Pred. No. 8.6e-05;
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                                                                                                                                                                                                                   Claim 18; Page 74; 102pp; English.
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                                                                                                          Mattsby-Baltzer I,
             98SE-0002441.
98SE-0002562.
98SE-0004614.
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98SE-0002562.
98SE-0004614.
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91.7%;
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                                                                          (ASCI-) A+ SCI INVEST AB.
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Best Local Similarity
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17-JJL-1998;
29-DEC-1998;
           06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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                                                                                                          Hanson LA,
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                numan; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                     New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
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Mattsby-Baltzer I, Baltzer L,
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98SE-0002562.
98SE-0004614.
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                                                              WPI; 2000-147388/13.
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ses 11; Conserv
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29-DEC-1998;
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Hanson LA,
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Matches
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urinary tract infections, colitis, and Candida infection on a mucosal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR98554 standard; Peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heat-resistant and water-soluble
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
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AAY78035
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AC AAY78
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                              AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food sutiffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 9.2e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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Claim 15; Page 75; 102pp; English.
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Best Local Similarity 91.7
Matches 11; Conservative
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17-JUL-1998;
29-DEC-1998;
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membrane), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have deelred anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 21; Length 14;
Pred. No. 9.2e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64; DB 17; Length 15;
Pred. No. 9.8e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-ulcer agent; low toxicity; stable; heat-resistant.
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Tue Dec

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Human lactoferrin derived peptide SEQ ID NO:35.
25-APR-2000 (first entry)
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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens

WO200001730-A1.

13-JAN-2000.

99WO-SE01230 06-JUL-1999; 98SE-0002441. 98SE-0002562. 98SE-0004614. 17-JUL-1998; 06-JUL-1998;

(ASCI-) A+ SCI INVEST AB.

Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 12; Page 69; 102pp; English.

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the circulation. A medical and are then transported through the circulation. A medical product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and candida infections (such as urinary tract infections, colltis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also con though native human lactoferrin have been shown to have dealred anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

Sequence

ö Query Match 97.0%; Score 64; DB 21; Length 15; Best Local Similarity 91.7%; Pred. No. 9.8e-05; Matches 11; Conservative 0; Mismatches 1; Indels

Search completed: February 21, 2003, 07:56:43 Job time : 28.093 secs

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seduence sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MASHIMA, SHUBKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TAWARA, SHUBYICHI
APPLICANT: KWAZAKI, YOSHIHIRO
APPLICANT: TYMAZAKI, YOSHIHIRO
APPLICANT: UNININI YURAL INPECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAMER: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: FJN-019
TELEBEROCHOCKET NUMBER: FJN-019
TELEBERATION NUMBER: 1248-700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRACTERISTICS:
LENGTH: 18 amino acids
WOTH.
                                   US-08-724-586-2
US-09-9221-632-2
US-08-655-640-2
US-08-655-640-4
US-08-461-333-4
US-08-461-333-4
US-08-461-333-4
US-08-476-798-4
US-08-476-798-4
US-08-455-106-2
US-08-455-108-2
US-08-455-108-2
US-08-455-108-2
US-08-455-108-2
US-09-456-108-2
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Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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STRANDEDNESS: sin
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STATE: MA
COUNTRY: USA
ZIP: 02109
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 RESULT 1
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                                                                                                                      February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3,
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Sequence 1
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/cgn2_6/prodata/11.aa/5B_COMB.pep:*
/cgn2_6/prodata/11.aa/6A_COMB.pep:*
/cgn2_6/prodata/11.aa/6B_COMB.pep:*
/cgn2_6/prodata/11.aa/6B_COMB.pep:*
/cgn2_6/prodata/11.aa/PcTUS_COMB.pep:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-07-755-161A-3

US-07-755-161A-3

US-08-204-487-1

US-08-204-487-1

US-08-206-771-25

US-08-311-984-25

US-08-311-984-25

US-09-508-734-4

US-09-508-734-4

US-09-508-734-4

US-07-55-161A-10

US-07-91-174-10

US-07-91-174-10

US-07-91-174-10

US-08-104-487-7

US-08-104-487-7

US-08-104-487-7

US-08-104-487-7

US-08-104-487-7

US-08-104-487-7
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                                                                                                                                                                                                                                                                                                                              262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                            US-09-743-107B-90
66
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                      1 CFQWQRXMRKVR 12
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Match Length
                                                                                                                                                                                                Fitle:
Perfect score:
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                                                                                                                                                                                                                                      Sequence:
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                                                                                                                         Run on:
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No.
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                 ZIP: 07601
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                                                                                               Gaps
                                                                                                                                                                                                                                                                  Sequence 8, Application US/08485948
Sequence 8, Application US/08485948
Settler No. 5855882
GENERAL INFORMATION:
APPLICANT: FONG MING LI
APPLICANT: HELEN VLASSRA
APPLICANT: HELEN VLASSRA
APPLICANT: ANTHONY CERAN
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                         Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
FILING DATE:
                                                       97.0%; Score 64; DB 1;
91.7%; Pred. No. 3.8e-05
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 2
Pred. No. 3.8e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLING APPLICATION: 436
PRIOR APPLICATION DATA:
PILOR APPLICATION DATA:
PILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTONNEY/AGENT INCORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/POCKET NUMBER: 947-1-00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTY: USA
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.0%;
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DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FRAGMENT TYPE: internal US-08-485-948-8
                                                       Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                  1 CFOWORXMRKVR 12
                                                                                                                                                                     1 CFOWORNMRKVR 12
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CFOWORNMRKVR 12

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Gegenere & Application US/06628380

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APPLICANT ULT YOUN MING
APPLICANT ULT YOUN MING
APPLICANT ULT YOUN MING
APPLICANT ULT YOUN
ANDERS OF SEQUENCES, 9
COUNTRY: USA
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COUNTRY: USA
COUNTRY
COUNTRY: USA
COUNTRY
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FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDCATION: 2
IDENITIEICATION METHOD:
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.0%; Score 64; DB 1; Length 20;
                                                                      US/07/755,161A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                    SOFTWARE: DisplayMile
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755
FILING DATE: 13910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: ATORNEYS
APPRICATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REPRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
      OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: the publication information authors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
CRCANBILE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-755-161A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                  ATTREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: Now Jersey
COUNTRY: USA
ZIP: 07601

ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/486,217
FILING DATE:
APPLICATION NUMBER: 08/489,217
FILING DATE:
APPLICATION NUMBER: 08/486,217
FILING DATE: APPLICATION: 1995
APPLICATION NUMBER: 08/486,217
FILING DATE: APPLICATION NUMBER: 08/486,217
ATTOCKON ENGRAPHICATION NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: 201 443-564
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Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Manoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB;
Pred. No. 3.8e-
0; Mismatches
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805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington CITY: Washington CITY: Washington COUNTRY: U.S.A. ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible
                         E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
TYPE: amino acidd
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-475-055-8
CORRESPONDENCE ADDRESS: ADDRESSE: Klauber &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRXMRKVR 12
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JS-07-755-161A-3
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IOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEMAURE:
LOCATION: 19
IDENTIFICATION: METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
MUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: YAMANOTO, NAOKI
APPLICANT: NAKASHMA, HIDEKI
APPLICANT: NAKASHMA, HIDEKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: KAWASAKI, YOSHHHIRO
APPLICANT: KAWASAKI, YOSHHHIRO
APPLICANT: KAWASAKI, YOSHHHIRO
APPLICANT: NANABKI, YOSHHHIRO
APPLICANT: NANABKO SEQUENCES:
ADRESSEE: PATENT ADMINISTRATOR, TESTA, HURMITZ &
ADDRESSEE: THIERAUUT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.0%; Score 64; DB 1; Length 20; 91.7%; Pred. No. 4.2e-05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRIE READMELE FORM:
COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FILING DATE: O2-MAR-1994
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
DOCUMENT NUMBER:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08204487; Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 91.7'
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQRXMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: M. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-08-204-487-1
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                                                                                        Indels
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US-07-891-174-3
US-07-891-174-3
Sequence 3, Application US/07891174
Sequence 3, Application Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESSE: Wenderoth, Lind & Ponack STREET: Wenderoth, Lind & Ponack STREET: Boof Sequence CITY: Weashington STATE: D.C.
CONFUTEY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SPERATING SYSTEM: MS-DOS
                                                             Best Local Similarity 91.7%; Pred. No. 4.2e-05; Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCETWARE: Displaywite
CURRENT APPLICATION DATA:
APPLICATION NDMBER:
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NOWBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INPORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acide TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN:
INDIVIDUAL ISOLATE:
DRVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL ITYPE:
CRLL INNE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                  1 CFOWORXMRKVR 12
                                                                                                                                                                              2 CFOWORNWRKVR 13
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Sequence 25, Application US/08256771

Sequence 25, Application US/08256771

GENERAL INFORMATION:
APPLICAMY: MAMORIA TOWITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Weahington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:

1 IDENTIFICATION METHOD:

1 OTHER INFORMATION: /note= "Cys residues are protected to OTHER INFORMATION: prevent disulfide bond"

US-08-256-771-25
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                                                                    Length 20;
                                                                        97.0%; Score 64; DB 1; 1
91.7%; Pred. No. 4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/256,771 FILING DATE: July 22, 1994
                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PELLING DATE: JULY 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAZTEN NUMBER: 33,867
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 25 SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: Information acids
TYPE: Information acids
TYPE: Information acids
TYPE: Information acids
                                                                Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                         1 CFOWORXMRKVR 12
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                                                                                                                                                                                                                                                                          2 CFÓWORNWRKVR 13
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Matches 11; Conserv
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US-08-256-771-25
       US-08-256-771-24
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US-08-381-984-24
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Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: MAMORY TOWITA et al.
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SECURNCES: 32
CORRESPONDENCES: Manderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
STATE: D. C.
COUWTRY: U.S.A.
ZIP: 20005.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97:0%; Score 64; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.2e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *PATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORWATION: /note= "Cys residues are linked by
OTHER INFORWATION: disulfide bond"
                                                                                                                                                                                                                                                                                                                                                                           /note= "ANTIBACTERIAL PEPTIDE DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION UNMERS:

APPLICATION NUMBER:

FILING DATE:

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION TO BE STATE OF STATE 
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    Telephone: 202-371-8850
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /
OTHER INFORMATION: D. 120.4487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQRXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ČFOWORNMRKVR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS-08-256-771-24
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Gaps

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RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Sequence 4, Application US/09508734
; Patent No. 642569
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION:
; TITLE OF INVENTION: useful microorganism thereof
; CURRENT APPLICATION NUMBER: PCT/KR99/00373
; PRIOR FILING DATE: 1999-07-14
; PRIOR PILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
LOCATION:
LOTIENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as a fragment thered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.0%; Score 64; DB 1; 1
illarity 91.7%; Pred. No. 4.2e-05;
Conservative 0; Mismatches 1.
                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYRE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Morderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
CLASSIPICATION 252
PRICA APPLICATION DATA:
APPLICATION NUMBER:
                    805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECHMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPAX:
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWORXMRKVR 12
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                                                    Washington
                                                                                       STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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IDBNIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.0%; Score 64; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.2e-05; Matches 11; Conservative 0; Mismatches 1; Indels
Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Ammoru TOMITA et al.
TITLE OF INVENTION: ANIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCES: 32
CORRESPONDENCES: Menderoth, Lind & Ponack
STREET: 805 Fitteenth Street, N.W., #700
CITY: Washington
CITY: Washington
STATE: D.C.
COUNTY: U.S.A.
ZIP: 20005
CONFUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IRM Compatible
COMPUTER: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFFCATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
APPLICA
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Patent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WATER M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REPERENCE/DOCKET UMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORXMRKVR 12
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US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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NAME/KEY: modified site
LOCATION: 21
LDENTIFICATION METHOD:
OTHER INFORMATION: Cyg residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cyg residue at location 4"
AUTHORS.
AUTHORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "thiol group of
Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 25;
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91.7%; Pred. No. 5.2e-05;
.ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10
                                                  ATTORNEY/AGENT INFORMATION:
NAME: WAZTEN M. CHEEK JY.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                   10:
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                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /not
OTHER INFORMATION: Cys
OTHER INFORMATION: thic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDENNESS SHIP
STRANDENNESS SHIP
TOPOLOGY: linear
MYDCTHETICAL:
ANTI-SENSE:
FRAGNENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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IMMEDIATE SOURCE:
LIBRARY:
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
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Patent No. 6423509

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: useful microorganism thereof

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 1999-07-14/RR99/00373

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 6

SEQ ID
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97.0%; Score 64; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 4.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 4; Length 24;
Pred. No. 5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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IS-07-755-161A-10
Sequence 10, Application US/07755161A
Patent NO. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Agent
TITLE OF INVENTION: Antimicrobial Agent
TITLE OF INVENTION: Antimicrobial Agent
ONNERSPONDENCE ADDRESS:
ADDRESSEE: Wendertch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: D.C.
COUNTRY: U.S.A.
ZIP: D.C.
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: MSA Compatible
COMPUTER: NSA Compatible
COMPUTER: NSA COMPATINE
OMERGINER: NSA COMETINE
OMETINER: NSA COMETINE
OMERGINER: NSA COMETINE
OMERGINER: NSA C
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 19910905
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Best Local Similarity 91.7
Matches 11; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
/ LENGTH: 22
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                     1 CFOWORXMRKVR 12
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Gaps ; 0

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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.0%; Score 64; DB 1; Length 25; 91.7%; Pred. No. 5.2e-05; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                         DATE:
DOCUMENT NUMBER:
FILING DATE:
FULLIG DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                      TITLE:
JOURNAL:
VOLUME:
ISSUE:
                                                                                                                                                                                                                                                                                                                     PAGES:
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                                       Sequence 10, Application US/07891174
Sequence 10. Application US/07891174
Sequence 10. Application US/07891174
Sequence 10. Application:
CEREAL INFORMATION:
MAMONIA MAINIAICADDIAL BEPLICANT:
NUMBER OF ENGURENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Menderoth, Lind & Ponack
STREET: BOS Fifteenth Street, N.W., #700
CITY: Washington
STREET: D.C.
COUNTRY: U.S.A.
ZIP: 20005
CONTRY: D.S.A.
ZIP: 20005
CONTRY: D.S.A.
APPLICATION NUMBER: US/07/891,174
FILING DATE: D.SAPL1992
CLASSIFICATION NUMBER: US CONTRY: D.SEP-1991
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: US CONTRY APPLICATION NUMBER: US CONTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
NAME/KEY:
OCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: (note-
OTHER INFORMATION: (rote-
OTHER INFORMATION: thiol (
FRATURE:
NAME/KEY: modified site
LOCATION: 21
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INDIVIDUAL ISOLATE:
DBVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LINERARY:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
CREAGMENT TYPE:
CREAMINAL SOURCE:
ORGANISM:
                                       JS-07-891-174-10
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ALIGNMENTS
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN RECOAL
APPLICANT: RALDUR SVEINBJ (RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.0%;
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Matches 11, Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-798-869-20
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Sequence 7, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 8, Appli
Sequence 29, Appli
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Sequence 47985,
Sequence 2, Appli
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                                                                                                            February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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Sequence 9, 7
Sequence 11,
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Sequence 3
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'Ggn2_E/ptodata/2/pubpaa/NET_NEW_PUB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/NEG_NEW_PUB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO6_NEW_PUB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO7_NEW_PUB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO7_NEW_PUB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO7_NEW_PUB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO8_PUBCOMB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO8_NEW_PUB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO8_PUBCOMB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO8_PUBCOMB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO8_PUBCOMB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO8_PUBCOMB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO8_PUBCOMB.ppp.*
'Ggn2_E/ptodata/2/pubpaa/USO8_PUBCOMB.ppp.*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-888-320-2
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US-09-798-869-20
US-09-798-869-3
US-09-798-869-3
US-09-798-869-7
US-09-798-869-7
US-09-798-869-22
US-09-798-869-22
US-09-798-869-22
US-09-798-869-22
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US-09-904-536-12
US-09-904-536-13
                                                                                                                                                                                                                                                                                                                              156504 segs, 31069816 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
Sequence:
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Maximum DB seq
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Sequence 14, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl	THE RE	27 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	<b>.</b> 40401	Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 28, Appl Sequence 24, Appl Sequence 21, Appli Sequence 4, Appli
US-09-904-536-14 US-09-904-536-15 US-09-904-536-16 US-09-904-536-16 US-09-904-536-17	US-09-904-536-10 US-10-095-449-6 US-09-448-378-1 US-09-983-806-6 US-09-904-536-1	US-09-738-626-5715 US-09-764-864-1031 US-10-051-409-4 US-10-090-453A-2	US-09-864-761-48879 US-09-824-588-2 US-09-864-761-44327 US-09-869-26	US-09-798-869-12 US-09-798-869-11 US-09-798-869-10 US-09-798-869-28 US-09-798-869-24 US-09-798-869-21 US-09-909-652-4
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Pred. No. 2.5e-05;
0; Mismatches 1,
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDEN
APPLICANT: JOHN SIGUED SVENDEN
APPLICANT: GYSTEIN REKDAL
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: AA4049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/7798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRANCES OF TOWN OF SEQ ID NOS: 30
SOFTWARE: PRICE WINDOWN OF SEQ ID NOS: 30
SOFTWARE
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Gaps

Length 694;

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Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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US-09-798-869-3
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; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
APPLICANT: KTUZEL, Marian L.
APPLICANT: GOIlnick, Paul D.
APPLICANT: GOIlnick, Paul D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: 8
COURTEST: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                           97.0%; Score 64; DB 9; Length 25; 91.7%; Pred. No. 4.1e-05;
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MEDIUM TYPE: Floppy disk COMPUTER IBM FC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATCHIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/023,096 FILING DATE: CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/724,586 FILING DATE: 30-SEPT-1996 APPLICATION NUMBER: US/08/724,586 FILING DATE: 05-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
              TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSECRE FOR WINDOWS Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REPRENCE/DOCKET NUMBER: 10501
TELECOMMUNICATION INFORMATION:
TELEPHORE: (202) 638-6666
TELEFAX: (202) 638-666
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acids
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Best Local Similarity 91.7
Matches 11; Conservative
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LARS VORLAND
                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapiens
US-09-798-869-20
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Pred. No. 0.00062;
0; Mismatches 2; Indels
97.0%; Score 64; DB 9; 31.7%; Pred. No. 0.00096; ive 0; Mismatches 1
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Pred. No. 0.0021;
                                                                                                                                                                                                                                                         Georgian of Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OGHN SIGURD SVENDSEN
APPLICANT: HALDUR SYBINGAL
APPLICANT: HALDUR SYBINGAL
APPLICANT: HALDUR SYBING (RNSON)
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
ITILE REPERBNCE: A34049-PCT-USA-A
CURRENT RILING DATE: 2001-02-27
CURRENT PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FABUSEQ for Windows Version 4.0
SSOFTWARE: FABUSEQ for Windows Version 4.0
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Sequence 3, Application US/09798869;
Publication No. USZ0030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON)
TITLE OF INVENTION: BIOACTURE PEFTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR PELING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9918938.4
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FEASTSC for Windows Version 4.0
SSC ID NO 3
LENGTH: 15
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.7%; Score 44; DB 9; Length 25; Best Local Similarity 63.6%; Pred. No. 0.12; Matches 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                      APPLICANT: OCHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPPLIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: CTJGB99/02851
PRIOR APPLICATION NUMBER: GB9818938-4
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 15
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PUBLICANT:
VEYTERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDEN
APPLICANT: JOHN SIGURD SVENDEN
APPLICANT: VEYTERN REXDAL
APPLICANT: BALDUR SVENDAD
ITILE OF INVENTION: BIOACTIVE PEPTIDES
ITILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02651
PRIOR APPLICATION NUMBER: PCT/GB99/02651
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARR: PARESQ for Windows Version 4.0
SSET DATE: 25
                                                                                                                                                       Sequence 4, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
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Best Local Similarity 63.6
Matches 7; Conservative
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1 CFQWQRXMRKV 11
                                          3 CYÓWOWRMRKL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: MURINE
US-09-798-869-22
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US-09-798-869-22
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Gaps
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OTHER INFORMATION: synthetic peptide (modified form of homo sapiens OTHER INFORMATION: sequence)
1S-09-798-869-7
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Pred. No. 0.0034;
2; Mismatches 1; Indels
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1; Indels
2; Mismatches
                                                                                                                                                  ESULT 6
19-09-798-869-23
Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SVENDEN
APPLICANT: (YSTEIN RENDAL
APPLICANT: 1ARS VORLAND
TILE OF INVENT SA404-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSESSEE OF Windows Version 4.0
SEQ ID NO 23
LENGTH: 25
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: ABADUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-06-31
PRIOR PILING DATE: 1999-06-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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ORGANISM: Artificial Sequence
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWORXMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CYOWORRMRKL 13
                                          CPOWORXMRKV 11
                                                                                     3 CYÓWÓRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: CAPRINE
IS-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESULT 7
Matches
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.1%; Score 41; DB 9; Length 15; 54.5%; Pred. No. 0.26; 2; Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.1%; Score 41; DB 9; Length 15; llarity 63.6%; Pred. No. 0.26; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-001-798-869-29
Sequence 29, Application US/09798669
FUBLICATION OF US20030022821A1
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: ALAS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
SQUENCE 8, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDEN
APPLICANT: APLICANT: BALDUR SVEINBU (RNSON)
APPLICANT: BALDUR SVEINBU (RNSON)
APPLICANT: BALDUR SVEINBU (RNSON)
APPLICANT: BALDUR SVEINBU (RNSON)
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR PLING DATE: 1999-08-31
PRIOR PLING DATE: 1999-08-31
PRIOR PLING DATE: 1999-08-31
PRIOR PLING DATE: 1999-08-31
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 54.5.
The G Conservative
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Best Local Similarity
Matches 7; Conserval
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; ORGANISM: BOVINE
US-09-798-869-29
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US-09-798-869-30
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LENGTH: 15
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LENGTH: 15
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Bavid R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David G.
APPLICANT: Chen, Wensheng
TITLE G. INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBER: US 60/180,312
READ PRICATION NUMBER: US 60/20-04
READ PRICATION NUMBER: US 60/20-04
PRICA APPLICATION NUMBER: US 60/20-05
PRICA APPLICATION NUMBER: US 60/20-05
PRICA APPLICATION NUMBER: POT/US01/0066
PRICA PRICA APPLICATION NUMBER: POT/US01/0066
PRICA PLING DATE: 2001-01-30
PRICA PLING D
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Pred. No. 0.26;
3; Mismatches 2; Indels
                                                                                                            APPLICANT: JOHN SIGGED SVENDSEN
APPLICANT: JOHN SIGGED
APPLICANT: JOHN SIGGED
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTURE PEPTIDES
FILE REFERENCE: A34049-FOT-UGA-9,
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: B989-08-31
PRIOR APPLICATION NUMBER: B989-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastERQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 15
TYPE: PRT
TYPE: PRT
CRGANISM: BOVINE
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Patent No. US20020048763A1
Application US/09798869
No. US20030022821A1
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Best Local Similarity 54.5.
Thes 6; Conservative
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APPLICANT: Bekker, Linda-Gail
APPLICANT: Bekker, Linda-Gail
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the APPLICANT: The Seprement of Health and Alman Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REPERENCE: 015280-413100US
CURRENT APPLICATION NUMBER: US/09/888,320
CURRENT FILING DATE: 2001-06-22
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OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
IS-09-888-120-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: MAP TO AL096701.14

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUE 1.00e-06

IS-09-864-761-47985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.1%; Score 37; DB 10; Length 21; Best Local Similarity 83.3%; Pred. No. 1.8; Matches 5; Conservative 1; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-02-1
PRIOR FILING DATE: 2000-06-21
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4985
IENGTH: 21
TYPE: PRI
OPPRAVE: PRI
OPPRAVE: REI
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PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VEY. 2.1
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1S-09-888-320-2
Sequence 2, Application US/09888320
Publication No. US20030013090A1
GENERAL INFERMATION:
APPLICANT: Barry III, Clifton E.
APPLICANT: DeBarber, Andrea E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5
Matches 6, Conservative
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LENGTH: 489
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ESULT 15 S-09-504-536-8 Sequence 8, Application US/09904536 Patent No. US20020111475A1

GENERAL INFORMATION

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APPLICANT: Graddis, Thomas J.
APPLICANT: McGraw, Jeffrey T.
ITLE OF INVENTION: FIT3-1 MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT PEPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION 09/109,100
PRIOR APPLICATION NUMBER: PRIOR PELING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTING DATE: 1999-07-02
SOFTWARE: 1999-07-02
SOFTWARE: 1999-07-02
SOFTWARE: 1999-07-02
SOFTWARE: 1999-07-07
SOFTWARE: 1999-07-07
SOFTWARE: 1999-07-07
SOFTWARE: 1999-07-07
SOFTWARE: 1999-07-07
SOFTWARE: 1
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F1511.22 [imported
pyridoxamine-phosp
                                                                                                                  February 21, 2003, 07:48:01; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                      fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                  283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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S07442
C86624
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Match Length DB
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1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:*
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Perfect score:
Sequence:
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No.
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fprA protein - Myx	hypothetical prote	cell cycle arrest	ornithine decarbox	probable cytochrom	cytochrome P450-li	cytochrome P450 ho	cytochrome P450-li	cytochrome P450 mo	hypothetical prote	hypothetical prote	finger protein unk	hypothetical prote	kinase-related pro	protein F21H11.2 [	carcinoembryonic a
T10126	AD2346	A39654	S52784	B96691	B85441	T04730	C85441	T52174	AB0858	T24218	842526	D83181	A35774	D88450	D33876
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53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	51.5
35	35	32	32	35	35	35	35	35	35	35	35	35	35	35	34
30	31	32	33	34	32	36		38	39	0.4	41	42	43	44	45

	ALIGNMENTS
	lactotransferrin precursor [validated] - human NyAlternate names: lactoferrin
	C;Spectes: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000 C;Accession: G01394: S11228: A45401; S10324: S15853: S20841: S07160: A61169: A31000: S74
_	A; Reference number: G06820 A; Accession: G01394
	A;Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: mRNA
	A A CONTRACT AND A CO
	Ajdross-references: Embilouvets; NID:94e/Z35; FIDN AABSO324.1; FID:94e/Z3/ R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pleper, F.R.
	Nucleic Acidis Res. 18, 5588, 1990
	Ajille: Compiece incieotide sequence of numen mammary grand iscoletinn. AjReference number: S11228; MUID:90384839; PMID:2402455
	A;Accession: S11228 A.Molania type: mpna
	A.F. S.
	A, Cross-references: EMBL:X53961; NID:934415; PIDN:CAA37914.1; PID:934416
	RyTeng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T. McT Endorwinch 6 1969-1981 1992
	A; Title: Differential molecular mechanism of the estrogen action that regulates lactofer
	A.Reference number: A45401; MUID:93125571; PMID:1480183
-	Aymolecule type: DNA
****	A; Residues: 1-15 <ten></ten>
	A/Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312
	Ajtxperimental Source placenta Ajtxperimental Source (Area Moet asset)
	A. NOCE: BEGGETTO CALLECTOR INCD. DAUGHOUSE (NODE: LEZZOZ) R. POWGLI, M.J.; Ogden, J. B.
	Nucleic Acids Res. 18, 4013, 1990
	AjTitle: Nucleotide sequence of Inman lactoferrin CDNA. AjReference number: S10324: WIID:9032649: PMID:2374734
	A, Accession: S10324
	A. Molecule type: "RNA A. Residina - 3-711 PD/W.
	A. Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
	Ristowell, K.M.; Fado, T.A.; Funk, W.D.; Tweedie, J.W.
	A; Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
	A;Reference number: S15853; MUID:91264786; PMID:2049066 A:Accession: S15853
	A; Status: nucleic acid sequence not shown; not compared with conceptual translation
	A;Molecule type: mkNA A;Residues: 20-31 <st1></st1>
	A/Accession: S20841
	A/MOLECULE (Type: process) A/Residues: 20-28/Y.30-31 <st2></st2>

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Gaps

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Length 708;

DB 2;

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80.3%; Score 53; DB ilarity 72.7%; Pred. No. 0.09 Conservative 2; Mismatches
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R;Liu, Y.; Teng, C.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYOWOKKOMRKL 29
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                                                                                                                                                                                                         38 CYQWQRRMRKL 48
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                                                              Best Local Similarity
Matches 8, Conserv
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A,Residues: 3-707 <PEN>
                                                                                                                                                1 CFQWQRXMRKV
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                               Query Match
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C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; drycoprotein; iron binding; milk
C;Superda: duplication; glycoprotein; iron binding; milk
C;Superda: signal sequence #status predicted <5G10>
F;20-711/Product: lactocransferrin repeat homology <TRH1>
F;20-69/Domain: transferrin repeat homology <TRH2>
F;36-69/Domain: transferrin repeat homology <TRH2>
F;36-65,39-56,135-218,177-193,190-201,251-2565,503-697,595-608/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                                                                          A; Molecule type: mRNA
A; Residues: 436-487,'A', 489-711 <RAD>
A; Residues: 436-487,'A', 489-711 <RAD>
A; Cross-references: EMBL: MR8642; NID:9186815; PIDN:AAA86665.1; PID:9386855
A; Cross-references: EMBL: MR8642; NID:91
Cancer Res. 51, 3037-3043, 1991
A; Ttele: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A; Reference number: A61169; MUID:91235214; PMID:1674448
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R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A;Accession: JC2323; MUID:94380047; PMID:8093048
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                                                                                                                                                                                                                                                                                                                                                                                                                              A; Wolecule type: protein
A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A; Rote: this is the final paper in a series
R; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Bur. J. Blochem: 241, 303-308, 1996
Bur. J. Blochem: 241, 303-308, 1996
A; Ritle: Lacroferrin: similarity to diamine oxidase and purification by aminohexyl affin A; Reference number: S74119; MUID:97054624; PMID:8898921
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; WUID:88001031; PMID:3477300
A;Accession: S07160.
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F:359-696/Domain: transferrin repeat homology <TRH2>
F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
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A;Residues: 1-708 <LEP>
C;Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                         A,Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: GDB:LTF
Cross-references: GDB:119368; OMIM:150210
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91.7%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
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NiAlternate names: lactotransferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A41205
R;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secriticis can unber: A92596; MUID:87280033; PMID:3611056
lactoferrin - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997

C;Accession: S52107

R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.

R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.

R;Qian, S.Y.; Jolles, P.; Migliore-Samour, D.; Jolles, P.; Migliore-Samour, D.; Migli
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J. Blol. Cham. 266, 1980-21885, 1991
A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; WUID:92042099; PMID:1939212
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:20-707/Product: lactotransferrin #status predicted <MAT>
:358-695/Domain: transferrin repeat homology <TRH2>
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A,Molecule type: protein
A,Residues: 1.33 <Q1AA
C,Superfamily: transferrin; transferrin repeat homology
C,Keywords: duplication
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A,Residues: 1-15 <LIU>
A,Cross-references
C,Superfamily: transferrin; transferrin repeat homology
C,Reywords: duplication; glycoprotein
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Pred. No. 0.016;
3; Mismatches
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beta heavy chain - Chlamydomonas reinhardtii

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A;Gene: CESP:F07C3.1
A;Map position: 5
A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599
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C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Date: 30-Sep-2001
R; Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; PMID:11743194
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell starp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ğ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
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A,Molecule type: DNA
A,Residues: 1-206 <KUR>
A,Residues: 1-206 <KUR>
A,Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
                                                                                                                                                                   A)Status: preliminary; translated from GB/EMBL/DDBJ
A)Solecule type: DNA
A)Residues: 1-932 - 248L-
A)Cross-references: EMBL-US0308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
A)Experimental source: strain Bristol N2; clone F07C3
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Pred. No. 25;
1; Mismatches 3; Indels
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R;Favello, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F07C3.
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A;Map position: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                            A; Reference number: Z20528
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A;Molecule type: DNA
A;Residues: 1-206 <KUR>
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                                                                                                                                    Cispecies: Chlamydomonas reinhardtii
Cibate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
Accession: T086030
Rimitchell, D.R.; Brown, K.S.
U. Cell Sci. 107, 635-644, 1994
A:Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A:Reference number: Z16302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Map position: IX

A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;

A;Introns: 48/2; 74/3; 105/3; 4240/3

3/34/3; 366/3; 386/2; 4240/3

C;Superfamily: dynein heavy chain, ciliary

C;Superfamily: dynein heavy chain, ciliary

C;Reywords: nucleotide-binding motif A (P-loop)

F;1919-1926/Region: nucleotide-binding motif A (P-loop)

F;2500-2537/Region: nucleotide-binding motif A (P-loop)
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Molecule type: DNA
;Residues: 1-275 <MIL.>
;Residues: 1-275 <MIL.>
;Cross-references: EMBL:281089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
;Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F53H4.4 - Caenorhabditis elegans
C;Spcides: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                           Status: translated from GB/EMBL/DDBJ
Molecule type: DNA
Residuce: 1-4568 -MIL:
Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
Experimental source: strain 21gr
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3;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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4,Introns: 67/1; 153/1
2,Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
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R;Dobson, R. submitted to the EMBL Data Library, October 1996 A;Reference number: Z19587

Accession: T22597

;Gene: CESP:F53H4.4

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hypothetical protein F07C3.1

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2; Length 289;

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Query Match
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R;Theologia, A.; Ecker, U.R.; Palm, C.U.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chinelogia, A.; Ecker, U.R.; Palm, C.U.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 409, 816-820, 2000

C.A.; Li, O.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziall, Rizzo, M.; Rowley, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Arlicle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G86403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, B.; Selkov, B.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - Brucella melitensis (s
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!Molecule type: DNA
| Residues: 1-208 <KUR>
| Cross-references: GB:AE008917; PIDN:AAL52699.1; PID:g17983525; GSPDB:GN00190
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A,Residues: 1-289 <STO>
A,GCOSe-references: GB.AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141
C;Genetics:
A;Cross-references: GB:AE008688; PIDN:AAL41776.1; PID:g17739129; GSPDB:GN00186
A;Experimental source: strain CS8 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Brucella melitensis
Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                    59.1%; Score 39; DB 2;
Larity 50.0%; Pred, No. 9;
Conservative 2; Mismatches 4
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                                                                                A,Gene: pdxH
A,Map position: circular chromosome
C,Superfamily: pyridoxamine-phosphate oxidase
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C;Superfamily: pyridoxamine-phosphate oxidase
C;Keywords: oxidoreductase
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Pred. No.
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Best Local Similarity 50.0
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-515 <ROU-
A; Cross-references: EMBL: AC002391; NID:g2642421; PID:g2642441
A; Cross-references: EMBL: AC002391; NID:g2642421; PID:g2642441
A; Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C;Accession: T00510; A84622
E;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau submitted to the EMBL Data Library, November 1997
A;Description: Arabidopsis thallana chromosome II BAC T20D16 genomic sequence.
A;Reference number: Z14164
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A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
K;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tailon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
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                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   - Arabidopsis thaliana
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Pred. No. 33;
1; Mismatches
Score 38; DB
Pred. No. 19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome P450 At2g23220 [imported]
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A;Molecule type: DNA
A;Residues: 1-543 <ROU>
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57.6%;
ilarity 50.0%;
Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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                                  Best Local Similarity
Matches 6; Conserv
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;Molecule type: DNA
;Residues: 1-515 <STO>
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Introns: 182/3; 310/3
                                                                                                                                               1 CPOWORXMRKVR
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A;Residues: 1-85 <PAR>
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;Keywords: chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regulat;
;65-581/Domain: phytochrome homology <PHY>
;321/Binding site: phytochromobilin (Cys) (covalent) #status predicted
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ih, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
dature 413, 848-852, 2001
%; Moule, S.; O'daora, P.
Athurhors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
Athurhors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
Y.Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy
%; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: T14803
:Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Fratt, L.H.; Morgan, P.W.; Mullet,
Dabmitted to the EMBL Data Library, April 1996
:Reference number: Z18186
ture 402, 761-768, 1999
Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                           Status: preliminary
Molecule type: DNA
Residues: 1-543 <STO>
Cross-references: GB:AE002093; NID:g2642444; PIDN:AAB87112.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Sorghum bicolor (sorghum)
Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
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%Introns: 211/3; 339/3

%Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

%Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

?;341-500/Domain: cytochrome P450 homology <P45>

?;478/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Best Local Similarity 83.3%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 0; Indels
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Molecule type: mRNA
Residues; 1-1135 cMls
Cross-references: EMBL:U56731; NID:g1800218; PID:g1800219
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A;Cross-references: GB:AL513382; PIDN:CAD07537.1; PID:g16503529; GSPDB:GN00176
C;Genetics:
A;Gene: pmrD
                                                                               Score 37; DB 2; Length 85;
Pred. No. 8.9;
1; Mismatches 3; Indels
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Best Local Similarity 60.0%;
Matches 6; Conservative
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SEQUENCE FROM N.A.
TISSUE=Mammary gland;
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SEQUENCE FROM N.A.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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## ALIGNMENTS

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Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
                                                                                                                21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferroxin A;
Lactoferroxin B; Lactoferroxin C],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB-Mammary gland;
MEDLINE-90384839; PubMed-2402455;
Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Mammary gland;
Liang Q., Jimenez-Plores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
TRFL HUMAN STANDARD, PRT; 711 AA.
P02788; Q16780; Q16786; Q16789; O00756; Q9H1Z3; Q96KZ4;
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Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Mammary gland; Cheng H., Chen X., Huan L.; "Cheng H., Chen X., Huan L.; "CDNA Cloning and sequence analysis of human lactofetrin."; submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conneely O.M.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
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McCombie W.R., Wilson R., Chen B., Gibbs R., Zuo L., Johnson D., McCombie W.R., Wilson R., Chen B., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansaria A., Mardis E., Schutz K., Chen C.N., Evans C., Fitzgerald M., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Glacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,
Submitted (MAR-1997) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
MEDLINE=90064528; PubMed=258556;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
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                                                                                                                                                                                                                        Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                              MEDLINE-82262043; PubMed-7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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MEDLINE-97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                 "The present state of the human lactotransferrin sequence. Study alignment of the cyanogen bromide fragments and characterization N- and C-terminal domains."; Biochim. Biophys. Acta 670:243-254(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031; PLDMed=3477300;
Rado T.A., Wel. X., Benz E.J. Jr. or
"Isolation of lactoferrin CDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-
                                                                                                                                                                                             PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE-82046817; PubMed=6794640;
                                                                                     SEQUENCE OF 20-711.
MEDLINE-85076667; PubMed=6510420;
MEDLINE-85076667; PubMed=6510420;
MEDLINE-85007667; Johnson J., Mazurier J., Schoentgen F., Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-FAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                    'An 88 amino acid long C-terminal sequence of human
           IISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
Powell M.J., Ogden J.E.;
NNuclectide sequence of human lactoferrin cDNA.";
Nucleic Acids Res. 18:4013-4013(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                      comparisons with other transferring.";
Eur. J. Biochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acta Crystallogr. D 51:629-646(1995)
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SEQUENCE OF 3-711 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                   lactotransferrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: TRANSPERRING ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.

FUNCTION: LACTOPERROXINS A, B AND C HAVE OPIOID ANTAGONIST ACTIVITY. LACTOPERROXINS A SHOWS PREPERRORE POR MU-RECEPTORS, WHILE LACTOPERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERRING FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Ifo K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived from human lactoferrin.";
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N., Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y., Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F., Hotta El Matri L., Iwata F., Kaier-Kupfer M., Nagata M., Nakayasu K., Hejtmancik J.F. Teng C.T., "Familial subpetitehal corneal amyloidosis (gelatinous drop-like corneal dystrophy): exclusion of linkage to lactoferrin gene."; Mol. Vision 4:31-32(1998)
                                                                                                                                                                                        MEDLINE=99192677; PubMed=10089508;
Jameson G.B., Anderson B.F., Norris G.B., Thomas D.H., Baker E.N.;
Structure of human apolactoferrin at 2.0-A resolution. Refinement
and analysis of ligand-induced conformational change.";
Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DAMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agric. Biol. Chem. 54:1803-1810(1990).
                                                                                                 Acta Crystallogr. D 55:403-407(1999).
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EMBL; U07643; AAB60324.1; -.
EMBL; M93150; AAA36159.1; -.
EMBL; M82202; AAA55511.1; -.
EMBL; M83205; AAA56656.1; -.
EMBL; M18642; AAA86665.1; -.
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X52941; CAA37116.1; -.
U95626; AAB57795.1; -.
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PubMed=9873069;
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1BKA; 08
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le Provost F., Nocart M., Guerin G., Martin P.,
"Characterization of the goat lactoferrin cDNA. Assignment of the
relevant locus to bovine Ul2 synteny group."

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-!- SUBGRILULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capra hircus (Goat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidaa; Caprina; Capra.
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Pred. No. 0.025;
1; Mismatches 2; Indels
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IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 6 (BY SIMILARITY).
ININED (GLUNAC...) (POTTON 1.1 (BY SIMILARITY).
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TISSIE-Mammary gland;
Lee T. S. Kim S. Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TREL CAPHI STANDARD; PRT; 708 AA. Q29477; Q29479; 15-D2C-1998 (Rel. 37, Last sequence update) 15-D2C-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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IISSUE-Mammary gland;
MEDLINE-94380047; PubMed=8093048;
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708 AA;
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Best Local Similarity
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TREL_CAPIT ID AC Q29477
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TISSUE-Mammary gland;

Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.F.;

Raramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.F.;

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

--- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSFORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

--- STUBUNIT: MONOMER (BY SIMILARITY).

--- SUBCINIT: MONOMER (BY SIMILARITY).

--- SUBCILILAR LOCATION: Secreted.

--- SUBCINIT: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

--- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Camelus dromedarius (Dromedary) (Arabian camel).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Somali; TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
int. Dairy J. 9:481-486(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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0
                  Score 64, DB 1, Length 711;
Pred. No. 0.00024;
0, Mismatches 1; Indels
                                                                                                                                                                                                                                                                                    TRFL CAMDR STANDARD; PRT; 708 AA. OSTUMO; Q9MZS5; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-UNN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin)
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LACTOTRANSFERRIN.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                   EMBL; U53857; AAA97958.1; --
BMBL; X78902; CAA55517.1; --
HSSP; O77699; ICE2.
InterPro; IPRO01156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00494; TRER, 2.
PROSTTE; PS00206; TRANSFERRIN.
PROSTTE; PS00206; TRANSFERRIN.
PROSTTE; PS00206; TRANSFERRIN. 2; 2.
PROSTTE; PS00206; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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L -> R (IN REF. 2).

C -> K (IN REF. 2).

F -> P (IN REF. 2).

S -> P (IN REF. 2).

S -> R (IN REF. 2).

D -> G (IN REF. 2).

W, PZEDBA3C83539960D CRC64;
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2. SIMILARITY.
BY SIMILARITY.
BY
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
LACTOTRANSFERRIN
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708 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92042099; PubMed=1939212;
MEDLINE=92042099; PubMed=1939212;
MILLY Y. Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885(1991)
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-LANGTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
-!- SUBUNIT: MONOWER.
-!- SUBCLIULAR LOCATION: Secreted.
-!- SUBCLIULAR LOCATION: Secreted.
-!- SUBCLIULAR LOCATION: TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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PIR, A28438, A28438.

RHSSP, P602788, LDf.

RMCD, MCI:96837; Lbf.

RICHEPTO, IPRO01156, Transferrin.

PRINTS, PR00422; TRANSFERRIN.

SMART; SMO0094; TRANSFERRIN.

PROSITE; P800206; TRANSFERRIN.

PROSITE; P800206; TRANSFERRIN.

R PROSITE; P800206; TRANSFERRIN.

PROSITE; P800207; TRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                           Mus musculus (Mouse).
Bykaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eurheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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LACTOTRANSFERRIN.
1.
   TRFL MOUSE STANDARD; PRT; 707 AA. P0071; P00
707 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, J03298; AAA40525.1; --
EMBL, BAB110; BAA13633.1; --
EMBL, BC006904; AAH06904.1; --
EMBL, M74778; AAA39427.1; --
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"Three-dimensional structure of mare diferric lactoferrin at 2.6-A
resolution.",
J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION. TRANSFRRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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COLLED COIL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COIL (POTENTIAL).
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                                                                                                                                                                                                                     EMBL, U02963; AAA19956.1; -.
InterPro; IPR004273; Dynein_heavy.
Effan, PF03028; Dynein_heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 1; Length 4568; Pred. No. 11; 3; Mismatches 3; Indels
    -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (AMW; 9A9AS393C7C36AE7 CRC64;
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Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 38, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
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-i- SUBGELULAR LOCATION: Secreted.
-i- COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SOMPLIARITY: BELONGS TO THE TRANSFERRIN PAMILY.
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Best Local Similarity
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"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes."
1. Sequence analysis of the Chlamydomonas alpha and beta dynein heavy call sci. "07.635-644(1994).
1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELIA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES. DYNEIN HAS ATPASE ACTIVITY.
1- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 35, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
0DA4 OR ODA-4 OR SUP1.
Eukaryota, Varidiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadacee; Chlamydomonads.
Chlamydomonadacee; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANION (POTENTIAL).

ALIUNKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MR -> IQG (IN REF. 1).
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F26AE0340A4C19A8 CRC64;
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IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
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63.6%; Pred. No. 1.1;
ive 1; Mismatches
2.
BY SIMILARITY.
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MEDLINE=94274778; PubMed=8006077;
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Best Local Similarity 63...
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707 AA;
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R PDB, 1BTX, 02-DEC-98.

R PDB, 1BTX, 02-EEB-99.

R PDB, 1BTZ, 02-EEB-99.

R InterPro, 1PR001156; Transferrin.

R Pfam; PR00405; transferrin; 2.

R PROSTITE; PR00205; TRANSFERRIN.

R PROSTITE; PS00206; TRANSFERRIN 1; 2.

R PROSTITE; PS00206; TRANSFERRIN 1; 2.

R PROSTITE; PS00206; TRANSFERRIN 3; 1.

R PROSTITE; PS00207; TRANSFERRIN 3; 1.

R PROSTITE; PS00207; TRANSFERRIN 3; 1.

R PROSTITE; PS00207; TRANSFERRIN 3; 1.

I NON TRANSFERRIN 3; 1.

SIGNAL 4.
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Pred. No. 9.3;
3; Mismatches 2; Indels
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hes 7; Conserv
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292 AA.

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NLA DROME STANDARD; 09XZL8; 09V391; 30-MAY-2000 (Rel. 39, Created)

NLA DROME ID NLA D AC Q9XZL DT 30-MA

RESULT 7

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STRAINBEACKALE NO. RAY.

RAY STRAINBEACKALE N. N. N.

RAY STRAINBEACKALE N. N. HOOKING R. A. GOCCAYNE J. D., Adame M. D., Calliker S. E. Holt R. A. Branch R. A., Galle R. F.,

RA Adame M. D., Calliker S. E. Holt R. A. Bobains R. A., Galle R. F.,

RA Amanatides P. G., Scherer S. E. II P. W. Hookins R. A., Galle R. F.,

RA Brandon R. C., Rogers Y. H. C., Elazej R. G., Chendre M., Henderson S. N.,

RA Brandon R. C., Rogers Y. H. C., Elazej R. G., Chendre M., Miklos G. L. G.,

RA Adam K. H., Doyle C., Barker B. G., Helt G., Nelson C. R., Miklos G. L. G.,

RA Barid J. F., Agbayan A., An H. J., Andrews-Febrankoch C. Baldwin D.,

Ballew R. M., Basu A., Berman B. P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D. A., Butler H., Cadieu E., Center A., Chandra I.,

Burtis K.C., Busam D. A., Butler H., Cadieu E., Dover P., Brottier P.,

Burtis K.C., Busam D. A., Butler H., Cadieu E., Dover B. C.,

Burtis K.C., Busam D. A., Bong Z., Mays A.D., Dew I., Dietz S. M.,

Gerry J. M., Canly F. D., Downes M., Deng Z., Mays A.D., Dew I., Dietz S. M.,

A Burtis K. Doug L. E., Downes M., Deng Z., Gand P., Bracker P., Eleis P.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J. R., Pleischmann W.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J. R., Plackom M.,

Adalali M., Kalush F., Karpen G. H., Wei M.-H., Ibegaman C.,

RA Harris N.L., Marter B., Wolnoch T.C., Morison J. M., Natherian D.,

RA Harris N.L., Marter D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Harris N., Mattel B. B., Wolnoch T.C., Morison J. M., Natherian G.,

RA Harris N., Mattel B. Wolnoch T.C., Morison J., Warry D. M., Natherian G.,

RA Harris M., Wow M., Murtow B., Nuxon K., Muszwitz D., Warry D., M., Natherian G.,

RA Harris M., Wow W., Murtow B., Nuxon K., Nusser D., Steneler F., Shen H.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri, V., Reading A., Wang Z.-Y., Wassarman D.A., Weinbecok G. M., Strong R., Spradling A.C., Staplecok M., Strong R., Strong R., Spradling A.C., Staplecok M., Strong R., Shen H., Sheng K., Mang Z.-Y., Wassarman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its modified mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                              NIA OR CG6072.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Bukaryota; Metazoa; Arthropoda; Mandibulata; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TAXID=7227;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
females.";
                                                                                                                                                                                                                                                                                                          Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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EMBL; AE003712; AAF55285.1; -.
FTyPasse; FBGNO26629; nla.
FEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
Last sequence update)
Last annotation update)
30-MAY-2000 (Rel. 39, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                           Nebula protein.
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SWART; SM00388; HisRA; I.
SWART; SM00086; PAC; 1.
SWART; SM00091; PAS; 2.
TIGREMMS; TIGRO0229; Sensory box; 2.
PROSITE; PS50109; HIS KIN; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS50046; PHYTOCHROME 1; FALSE_NEG.
PROSITE; PS50046; PHYTOCHROME 2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                            618 688 PAS 1.
748 822 PAS 2.
902 1122 HISTIDINE KINASE.
321 321 CHROWOPHORE (BY SIMILARITY).
1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;
SMART; SM00387; HATPase_c;
                                                                                                                                                                                            Repeat, Multigene family. DOMAIN 618 688
                                                                                                                                                                                                                                                                                                                                                              4; Conservative
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Best Local Similarity
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                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phytochrome B.";
Plant Physiol. 113:611-619(1997)
Plant Physiol. 113:611-619(1997)
Plant Physiol. 113:611-619(1997)
Plant Physiol. 113:611-619(1997)

ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
MAXIMALLY IN THE RAD REGION OF THE SPECTMM AND THE PRF FORM THAT
ABSORBS MAXIMALLY IN THE FAA-RED REGION. PHOTOCONVERSION OF PR IN
PFR INDUCES AMAXIMALLY IN THE FAA-RED REGION. PHOTOCONVERSION OF PR IN
PFR INDUCES AMAXIMALLY THE FAA-RED REGION. PHOTOCONVERSION OF PR IN
RESPONSES. PRR CONTROLS THE EXPERSION OF A NUMBER OF NUCLEAR
GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
BISCHOSPHATE CARROXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
PROTOCILOROPHYLLIDE REDUCTAGE, RENA, FEEDBACK PASHION (BY
                                                                                                                                                                                                                                                                                                                                                            Eukāryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lilliopsida, Poales, Poaceae, PACC clade,
Panicoideae, Andropogoneae, Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-i- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILIA.
-i- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-i- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (FAC) DOMAIN.
-i- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97198556; PubMed=9046599;
Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Millet J.B.,
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
     Score 38; DB 1; Length 292;
Pred. No. 6;
                                           3; Indels
                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                              PRT; 1135 AA
   Query Match
Best Local Similarity 54.5%; Pred. No. 6;
Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                            Sorghum bicolor (Sorghum) (Sorghum vulgare)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U56731; AAB41399.1; InterPro; IPR03594; ATPbind ATPase. InterPro; IPR003018; GAF.
InterPro; IPR004359; HIS KIN sig. InterPro; IPR004359; HIS KIN sig. InterPro; IPR001610; PAC. InterPro; IPR001610; PAC. InterPro; IPR0010194; PAS. domain. InterPro; IPR001294; Phytochrome; Pfam; PF00350; phytochrome; 1. Pfam; PF00959; PAS. 2. Pfam; PF00959; PAS. 2.
                                                                                                                                                                                                            STANDARD;
                                                                                                 150 FQWLRSFRRLR 160
                                                                             2 FOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                          Phytochrome C.
                                                                                                                                                                                                          PHYC SORBI
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Gaps

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Score 38; DB 1; Length 1135; Pred. No. 23; 4; Mismatches 3; Indels

57.6%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:852-856(2001)
-!- FUNCTION: CONFERS RESISTANCE TO POLYMXXIN B. POLYMXXIN RESISTANCE
MAY BE MEDIATED BY AN INTERACTION BETWEEN PMRA OR A PMRA-REGULATED
GENE PRODUCT AND PMRD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=Z1534948; PubMed=11677609;
MEDLINE=Z1534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                         Roland K.L., Bether C.R., Spitznagel J.K.; mrD selmonella "Isolation and characterization of a gene, pmrD, from Salmonella ryphimurium that confers resistance to polymyxin when expressed in multiple copies."; Dacteriol. 176:3589-3597(1994).
                                                                                                                                                                                                                                         Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                       01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-UWN-2002 (Rel. 41, Last annotation update)
POLYMYXIN B resistance protein pmrD.
                                                                                                    85 AA
                                                                                                                                                                                                                                                                                                                                                                      STRAIN=LT2;
MEDLINE=94266712; PubMed=8206837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U02281; AAA21322.1; -
                                                                                                      STANDARD;
775 CLEWNKAMOKI 785
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Pfam; PF02518; HATPase c; 1. PRINTS; PR01033; PHYTOCHROME. SMART; SM00065; GAF; 1.

us-09-743-107b-90.rsp

235 AA.

PRT;

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Page

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STANDARD;
FL3L_HUMAN
P49771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Nelaboruit,
STRAIN-Nelaboruit,
STRAIN-Nelaboruit,
Planet P., Jagounis S., Bove J.M., Garnier M.;
Detection and characterization of the African Citrus Greening
Liberobacter by amplification, cloning and sequencing of the rplKaJL-
rposC operon.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTIO
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRAITS.
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last ennotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {RNA}(N).
-!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA' CHAIN.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
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                                                                                                                                                             Score 37; DB 1; Length 85; 
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS01166; RNA POL BETA, PARTIAL.
Transferase, Transcription, DNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                            StyGene; SG10304; pmrD.
Antibiotic resistance; Complete proteome.
SEQUENCE 85 AA; 9749 MW; 1E1922419EA50CCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.1%; Score 37; DB 1; 60.0%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 AA.
                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                 56.1%;
60.0%;
       EMBL; AE008803; AAL21205.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U09675; AAA19557.1; -
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                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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PROSITE; PS01166; RNA
                                                                                                                                                                                                 Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                  1 CFQWQRXMRK 10
                                                                                                                                                                                                                                                                                                                                                                  74 CDEWORLTRK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPOB LIBAF
P41187;
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                                                                                                                                                                        Query Match
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ò 엄 RESULT 11 FL3L\_HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
secreted (isoform 2).
-i- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here) and 2/soluble; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bundles and cystine knots.";
Nat. Struct. Biol. 7:486-491(2000).
-!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYDERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.
-!- SUBUNIT: Homodimer (isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bgcobar S.; "Rtructural analysis of human and murine flt3 ligand genomic loci.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004213; Flt3_lig.
Pfam; PF02947; flt3_lig; 1.
Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-94235842; PubMed-8180375; Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Brobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.; Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoietic progenitor cells."; Blood 83:2795-2801(1994).
                                                      01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3
                                                                                                                                                                                                                                                                                                                                                                                                     ō
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Handle C. Culpepper J., Campbell D., McClanahan T., Zurawski S.,

Handle C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,

Bazan J.F., Kastelein R., Hudak S., Magner J., Mattson J., Luh J.,

Buda G., Martina N., Peterson D., Menon S., Shanafelt A.,

Muench M., Kelnar G., Manikawa R., Rennick D., Roncarolo M.G.,

Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,

Ligand for FILJ-FLKZ receptor tyroaine Kinase regulates growth of

haematopoietic stem cells and is encoded by variant RNAs.",
                                                                                                                                                                      Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20343011; PubMed=10881197;
Savvides S.N., Boone T., Karplus P.A.;
"Flt3 ligand structure and unexpected commonalities of helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=96032581; PubMed=7566977;
Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, U04806, AAA17999.1; -. EMBL, U03858; AAA19825.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U29874; AAA90949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene 11:1165-1172(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1ETE; 09-JUN-00.
Genew; HGNC:3766; FLT3LG.
                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                  (F1t3L).
                                                                                                                                                                                                                  NCBI_TaxID=9606;
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TISSUE=T-cell;
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P26898;
                                                                                                                          CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                           SIGNAL
                                                                                                                                                                                                                DOMAIN
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IL2A_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab.sib.ch).
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YOO J., de Leon F.A., Stone R.T., Beattie C.W.;
YOO J., de Leon F.A., Stone R.T., Beattie C.W.;
receptor alpha (IL-2R alpha) gene.";
Mamm. Genome 6.751-753(1995).
-!- FUNCTION: RECEPTOR FOR INTERLEUKIN, 2.
-!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
REAST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERREDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (LALPHA AND INTERMEDIATE AFFINITY MONOMER (BETA CHAIN).
MITH A GAMMA CHAIN.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
DN-LINKED (GLCNAC. .) (POTENTIAL).
DSSTLEPPWSRRELEATA -> VETVFHRVSQDGLDLLTS
(IN ISOFORM 2).
(IN ISOFORM 2).
G -> A (IN ISOFORM 2).
G -> A (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=88212503; PubMed=2835311;
MedLinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
Meeves R., Magnuson J.A.,
"Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
Immunology 63:603-610(1988).
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
11cerleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PS5) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                      DB 1; Length 235;
                                                                                                                                                                                                                                                                                                                      4; Indels
                  SL CYTOKINE.
EXTRACELLULAR (POTENTIAL).
                                                      POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                    54.5%; Score 36; DB 50.0%; Pred. No. 11;
   POTENTIAL
                                                                                                                                                                                                                                                  26416 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M20818; AAA51414.1; -. EMBL; U24226; AAC48487.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50...
Fac 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          204 CLHWORTRRR 213
                                                                                                                                                                                                                                                235 AA;
                                                                                                                                                                                                                                                                                                                                                          1 CFOWORXMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                179
                                                                                                                                                                             161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L2A BOVIN
                                   DOMAIN
TRANSMEM
DOMAIN
DISULFID
                                                                                                       DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein, CD25.",

Gene 113:283-284(1922).

Gene 113:283-284(1922).

- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R

- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R

EXIST IN 3 DIFFERENT FORMS: A HIGH APPINITY DIMER, AN INTERMEDIATE

AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA

CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE

WITH A GAMMA CHAIN.

-! SUBCELLULAR LOCATION: Type I membrane protein.

-! SUBCELLULAR CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92241682; PubMed=1572550;
Bujdoso R., Sargan D.R., Williamson M.L., McConnell I.;
Eloloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
protein, CD25.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,

Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-FBE-1996 (Rel. 33, Last annotation update)
11-FBE-1996 (Rel. 31) Last annotation update)
11nterleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PS5) (TAC antigen) (CD25).
                                                                                                                                           INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                  BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL)

N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                      Glycoprotein; Receptor; Repeat; Signal; Sushi
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 1; Length 275; Pred. No. 13; 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Verhagen A.A.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                        4901BBF9A4862390 CRC64;
                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 AA
                                                                                                                                                                                                                           SUSHI 1.
SUSHI 2.
PIR; SO7442; S07442.
HSSP; P01589; IILM.
INCEPERO; IPRO00436; Sushi_SCR_CCP.
Elam; PF00084; sushi; 2.
SMART; SM00032; CCP; 2.
Transmembrane; Glycoprotein; Recept
                                                                                                                                                                                                                                                                                                                                                                                            31238 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 CLIWORKWKKNR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWQRXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                         109 1
275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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ATX1 ARATH
Q9LT02;
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CONFLICT
SEQUENCE
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DOMAIN
DOMAIN
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BINDING
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ATX1 ARATH
ID ATX1 AS
AC 091702
DT 16-0CT
DT 16-OCT
DE POTENT
GN ATSC23
OC BURALY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Tahir M., Kanegae H., Takano M.;
"Phytochrome C (PHYC) gene in rice: isolation and characterization of a complete coding sequence.";
(In) Plant Gene Register PGR98-210.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE OF 275-378 FROM N.A.
MEDLINE=97019052; PubMed=8865668;
Mathews S., Sharrock R.A.;
Mathews S., Sharrock R.A.;
"The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
SUSHI 1.
SUSHI 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
S -> T (IN REF. 2).
W, 1101A2DE5ACSA088 CRC64;
                                                                                                               Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
SIGNAL
1 21 27
SIGNAL 22 275
INTERLEUKIN-2 RECEPTOR ALPHA CHAIN
DOMALN 22 243
EXTRACELLULAR (POTENTIAL).
TRANSMEM 244 262
POTENTIAL.
                                                                                                                                                                                                                                                                                                                ..
0
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PHYC ORYSA STANDARD;

ID FHYC ORYSA STANDARD;

AC Q9ZWĪ9; P93429;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

'6-OCT-2001 (Rel. 41, Last annotation update)
      EMBL; Z11560; CAA77652.1; --
EMBL; X60149; CAA4723.1; --
EMBL; X19167; CAA01447.1; --
FIR; S18910; S18910.
FIR; S18919; S18930.
FIR; J18999; S18899.
FIR; J01113; J01113.
HSSP; P01589; ILIM.
INTERPO; IPRO0048; Sushi SCR_CCP.
Ffam; PPO0064; sushi; 2.
SWART; SMO0032; CCP; 2.
                                                                                                                                                                                                                                                                    30904 MW;
                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                261 CLTWORRWKKNR 272
                                                                                                                                                                                                                                                                                                                                   1 CFOWORXMRKVR 12
                                                                                                                                                                                                                                                           166 1
275 AA;
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Best Local Similarity
Matches 6; Conserv
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Mol. Biol. Evo
                                                                                                                                               DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DISULFID
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CARECHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(8) IN A NEGATIVE FEEDBACK FASHION.

-!- STRICALLY HOMODIMER (BY SIMILARITY).

-!- SIMILARITY: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

-!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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16-0c7-2001 (Rel. 40, Last annotation update)

16-0c7-2001 (Rel. 40, Last annotation update)

Potential cation-transporting ATPase (EC 3.6.3.-).

ATSG23540 OR MQWI.11.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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824 PAS 2.

124 HISTIDINE KINASE.

322 CHROMOPHORE (BY SIMILARITY).

279 F - S (IN REF. 2).

292 C - S (IN REF. 2).

2125982 MM, P2AS20191CFE7B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB018442; BAA74448.1; -.
EMBL; U61207; AB481996.1; -.
Interpro; IPR003594; APbind_ATPase.
Interpro; IPR003018; GAF.
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36.4%;
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292 29
1137 AA;
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ses 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0119; CATATPASE.
PROSITE; PS00154; ATPASE_E1_E2; 1.
Mydrolase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                       SEQUENCE FROM N.A.
STRAIN=cv. COlumbia;
MEDILISE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                POLY-LYS.
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Length 1179;
Pred. No. 56;
3; Mismatches 2; Indels
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MAGNESIUM (BY SIMILARITY).
W; 4A3E82D2222A4D78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR001454; Hlgnase/hydrlase.
(Eam; PF00122; B1-E2 ATPase; 1.
PEam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131115 MW;
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816 81
1179 AA;
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SEQUENCE
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TRANSMEM
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MOD RES
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1144 CYSWERLLR 1152 쉄 Search completed: February 21, 2003, 07:51:37 Job time : 5.2093 secs

1 CFQWQRXMR 9

Query Match
Best Local Similarity 44.4%;
Matches 4; Conservative

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Gaps

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Q9cons arabidopsis

Q2185 arabidopsis

Q22185 arabidopsis

Q22186 lycopersico

Q98x36 salmonella

Q99qc0 human immun

Q99qb0 human immun

Q99yl17 human immun

Q94yl17 human immun

Q94yl17 human immun

Q94bl2 human immun

Q94bl2 human immun

Q94bl2 arabidopsis

Q91mal arabidopsis

Q91mal arabidopsis

Q91mal arabidopsis

Q91mg arabidopsis
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 296m21 homo sapien
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
12-Croctransferrin.
13-Croctransferrin.
14-Mo appiens (Human).
15-Marayota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 89.4%; Score 59; DB 4; Length 711; Best Local Similarity 90.9%; Pred. No. 0.0067; Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Straubberg R., Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 711 AA.
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                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                Q9YIJZ
Q9Q9L0
Q8Q454
Q8U6K3
Q9A6E4
Q44473
Q9NZW3
P96223
                                                                                                                                                                                                                                                                                                       08SQ16
09FH19
091MQ5
09ZTP0
                                                            Q8Z536
Q9YQC1
Q9YQC0
Q9YQB9
Q9YQB8
Q9YJI7
                                                                                                                                                                                                                                                           Q9HPA3
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Q8SRG3
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                                                PRELIMINARY;
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SEQUENCE FROM N.A.
TISSUE=PROSTATE;
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Qercb2;
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Q8TCD2
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Q9UCYS
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Q9tcd2 homo sapien
Q9tcd0 oviz aries
Q9xxd5 oryza sativ
Q9xhp1 sesamum ind
Q9xhp1 sesamum ind
Q19150 caenorhabdi
Q19153 caenorhabdi
Q1956 or hizobium 1
Q8ubc2 agrobacteri
Q9xr8 rhizobium m
Q9xr8 rhizobium m
Q8xe2 ralstonia s
Q8xex2 homo sapien
Q77855 human immun
Q77855 human immun
                                                                                           (without alignments)
114.078 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                              February 21, 2003, 07:44:43; Search time 21.6744 Seconds
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         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q9UCY5
Q9TC80
Q9XFD5
Q9XFD5
Q9XFD5
Q98C0
Q8UHC2
Q98CN9
Q8YFX3
Q8XSE2
Q8YFX3
Q8XSE2
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Q77855
Q77856
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Gapop 10.0 , Gapext 0.5
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sp_rvirus:*
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sp_baccraia:*
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sp_human:*
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sp_bhage:*
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sp_rodent:*
sp_rinus:*
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Maximum DB seq length: 2000000000
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SIGUENCE FROM N.A.
STRAIN=TAINAN 1;
MEDLINE=ZOVA970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
"Molecular cloning of 11S globulin and 2S albumin, the two major seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sesamum indicum (Oriental sesame) (Gingelly).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
genes that are differentially expressed at rice young panicle."; submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE CYTOCHROWE P450 FAMILY.
EMBL, AP140486; AAD29699.1; -.
InterPro: IPRO01128; Cytochrome_P450.
Pfam: PF00.067; P450.
PRINTS; PR00385; P450.
PROSITE; P800086; CYTOCHROME P450; UNKNOWN_1.
Heme: Monoxygenase; Oxidoreductase.
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                                                                                                                                                                                                                                                                                                                                                                                                      62.1%; Score 41; DB 10; Length 105; 60.0%; Pred. No. 2.3; 2; Indels tive 2; Mismatches 2; Indels
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SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE 105 AA; 11912 MW; BOEEFCDD487E19F9 CRC64;
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Last annotation update)
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01-ANG-1999 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F53H4.4 protein.
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J. Agric. Food Chem. 47:4932-4938 (1999).
EMBL; AF091841; AAD42943.1;
InterPro; IPR003612; AAI.
InterPro; IPR000617; Nagin.
InterPro; IPR001768; Try/amyl inhbtr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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PRINTS; PR00496; NAPIN.
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Best Local Similarity 66.,
Est Gi Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CPÓWERLGKK 70
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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AC 093.71
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome P40 (Fragment).
Cytochrome P40 (Fragment).
Eukaryora, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                            Sato I.;
"Characterization of the 84-kDa protein with ABH activity in human seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-MAGGENER (Sheep).
Distaryota; Metazos; Chordats; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovie.
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TISSUB-PANICLE:
Liu J. Yang J.;
"Suppression subtractive hybridization (SSH) identified candidate
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0
   Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%; Score 55; DB 4; Length 38; 90.9%; Pred. No. 0.0019; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                            Interpro; IPR001156, Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402P490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95127729; PubMed=7827104;
Johan Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
HSSP, 077698; ICE2.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
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                                                                                        SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
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les 7; Conservative
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Q9TR80

RESULT 3 Q9TRB0

Matches

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Q9XPD5

RESULT 4

Matches

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none;

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FIRATN=MAPF303099;
MEDLINE=21082930; PubMed=11214968;
Raneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Katanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.,
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Sacnphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley P., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                  Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyridoxamine 5'-phosphate oxidase.

PDXH OR ATU0760 OR AGR C 1381.
Agrobacterium tumefaciene (etrain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.1%; Score 39; DB 16; Length 205;
larity 50.0%; Pred. No. 11;
Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
                                   01-00T-2001 (TrEMBLrel. 18, Created)
01-00T-2001 (TrEMBLrel. 18, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Pyridoxamine 5'-phosphate oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBUHC2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 7:331-338(2000).
EMBL, AP003011; BAB53553.1; -...
InterProv, IRRO0659; Pyridox.oxidase.
Pfam; PF01243; Pyridox oxidase; 1.
ProDom; PD006312; Pyridox oxidase; 1.
IIGRFAMs; TIGR00558; pdxH; 1.
PROSITE; PS0164; PYRIDOX OXIDASE; 1.
PRT;
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  PRELIMINARY;
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Matches 6; Conserv
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                                                                                                                                                                                                NCBI_TaxID=381;
                                                                                                                                                                                                                               SEQUENCE
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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"Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
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                                                                                                                                               "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                 60.6%; Score 40; DB 5; Length 275;
63.6%; Pred. No. 9.7;
tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.6%; Score 40; DB 5; Length 932; 63.6%; Pred. No. 34; ive 1; Mismatches 3; Indels
                                       Dobson K.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Direct Submission.",
Submitted (UL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 105308; AGC42025.1, -.
INTERPORTING: PS50156; SSD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
Favallo A., Gattung S.;
"The sequence of C. elegans cosmid F07C3.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 932 AA; 105144 MW; 66680619ADACBFDS CRC64;
                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281999; CAB03137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              019153 PRELIMINARY, PRT, 932 AA. 019153, 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical 105.1 kba protein.
                                                                    [2]
SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] —
SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 63.0.
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                                                                                                                                                                                                                                                                                                                                             2 FOWORXMRKVR 12
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Waterston R.;
            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A. MEDLINE=21608551; PubMed=11743194;

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Gaps

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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

REATM=16M ATCC 23456 / BIOTYPE 1;

RX MEDLINE=20020109; Pubmed=11756688;

RA DelVecchio V.G., Kapatral V., Redkar R.J., Pykidis A., Reznik G.,

RA Juahonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

RA Juahonski L., Larsen N., O'Callaghan D., Letesson J.-J.,

RA Haselkorn R., Kyrpides N., O'Verbeek R.;

RA Haselkorn R., Kyrpides N., O'Verbeek R.;

RY Hre genome sequence of the facultative intracellular pathogen

RT Brucella melitensis.";

RT Brucella melitensis.";

RT Brucella melitensis.";

BR SEMBL, ABC09587; AAL52698.1;

DR PRDDOM; PO006312; Pyridox_oxidase.

ProDom; PO006312; Pyridox_oxidase;

RY ProDom; PO006312; Pyridox_oxidase;

RY ProDom; PO006312; Pyridox_oxidase;

RY MY CXIGORGES PAA; CSUNDASE;

RY Oxidoreductase; Complete Protecome.

SEQUENCE 208 AA; 23866 NW; CBIF50BC9612DE28 CRC64;
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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        01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31541 MW; ABB38818004B2EDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ICC protein homolog.
ICC OR RSP0534 OR RS00414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ralstonia solanacearum (Pseudomonas solanacearum).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 AA
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InterPro; IPR004844; S/T phosphtse.
Pfam; PF00149; Metallophos; 1.
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MEDLINE=21681879; PubMed=11823852;
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SEQUENCE 279 AA; 31541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                        Brucella melitensis.
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nes 6, Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=305;
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Q8XSE2
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STRAIN=1021,
STRAIN=1021,
STRAIN=1021,
STRAIN=2021,
STRAI
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurcollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk C., Epppas P., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., fe plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Scrib Coccente C24:1233-2328(201).

EMBL, AB009043; AAK86569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
(EC 1.4.3.5).
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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                                                                                                                                                                                                                                                                                                          Complete proteome.
SEQUENCE 206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;
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SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;
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Last seguence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 6; Conserv
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les 6, Conserv
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**Q92RH8** 

RESULT 10 Q92RH8

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OBYFK3

RESULT 11 Q8YFK3

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Best Loc Matches

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Search completed: February 21, 2003, 08:00:44 Job time : 22.6744 secs
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SEQUENCE
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Q77855;
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A ISOGAI T., OLA T., HAYASHI K., Sugiyama T., Otsuki T., Suzuki Y.,

A ISOGAI T., OLA T., HAYASHI K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,

A Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

A Matanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

A Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

A Ninomiya K., Iwayanagi T.;

T. Mishikawa T., Masuho Y.,

T. Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK002037; BAA92048:1; -.
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                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ11175.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Eutheria; Primates; Cararrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 11, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ1175 fis, olone PlACB1007375, weakly similar to phorbol ester/diacylglycerol-binding protein UNC-13.
HOMO sapiens (Human).
Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 59.1%; Score 39; DB 4; Length 306; Best Local Similarity 55.6%; Pred. No. 17; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Straubberg R.;
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC025708, AAH25708.1;
Hypothetical protein.
SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
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INTERPORT TRR000008, C2.

INTERPORT TRR0000009, C2, C3, C3, C4, C2 DOMAIN.

SMART; SM00339, C2, 1.

PROSTITE; PS00439, C2, DOMAIN. 1; UNKNOWN. 1.

PROSTITE; PS000030, RRW RNP 1; UNKNOWN. 1.

PROSTITE; PS000030, RRW RNP 1; UNKNOWN. 1.

SEQUENCE 466 AA; 53192 MW; E4113Ā5062F5BDEE CRC64;
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                                                       244 CFOWEKGTRIAK 255
1 CFOWORXMRKVR 12
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Q9NUS2;
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EMBL: Z47867; CAA87881.1; -. InterPro, IPRO00777; GP120. Pfam, PRO0516; GP120.

Fam, PRO0516; GP120.
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                            DB 4; Length 466;
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                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                             91 AA.
                         59.1%; Score 39; DB 55.6%; Pred. No. 26; iive 2; Mismatches
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Query Match
Best Local Similarity 55.0-
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Best Local Similarity 60.0
Matches 6; Conservative
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67 QWNRTLQKVR 76
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Hanson LA, Mattsby-Baltzer I,
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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                                                                                                                     February 21, 2003, 07:37:21 ; Search time 28.093 Seconds (without alignments) 56.918 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_101002:*

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqgreneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseqgreneseqp-embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseqgreneseqp-embl/AA1984.DAT:*
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5.1.3
Compugen Ltd.
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  GenCore version
Copyright (c) 1993 - 2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
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AAY78038
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Gapop 10.0 , Gapext 0.5
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1 CFQWKRNMRKVR 12
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Match
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Perfect score:
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Human lactoferrin	ซ	actof	Human lactoferrin	Advanced glycosyla	lac	Amino acid sequenc	n lacto	Anti microbial pep	-re				w		14	Anti-parasitic lac	Anti-parasitic lac	Peptide for anti-u	rrin	Lactoferrin-derive	Lactoferrin derive	Lactoferrin-derive	Lactoferrin-derive	Lactoferrin deriva	Anti-parasitic pep									
AAY78050	AAR98554	AAY78035	AAY78062	AAY78063	AAY78031	AAY78064	AAY78065	AAY78034	AAY78066	AAY78067	AAR69352	AAW13397	AAY78033	AAY68867	AAY78032	AAR21810	AAR44841	AAR48530	AAR48531	AAR57461	AAR57462	AAR84698	AAR84699	AAR80263	AAR80264	AAR98553	AAR91852	AAW03045	AAR90607	AAR87621	AAR87622	AAW26150	AAW14036	ALIGNMENTS
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414	94.4	4	4	94.4	94.4	94.4	94.4	94.4	4	411	4	4	d,	4	44	57	94.4	57	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4				94.4	94.4	94.4	94.4	
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11	13	14	15	. 16	17	18				22				56		28	29	30	31	32	33	34	35	36	37	38	გ	40	41	42	43	44	45	

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative. Human lactoferrin derived peptide SEQ ID NO:91. AAY78091 standard; Peptide; 12 AA. 98SE-0002441. 98SE-0002562. 98SE-0004614. 99WO-SE01230 (first entry) (ASCI-) A+ SCI INVEST AB.

Result No.

2 6 4 5 9 7 8 9 9

Dolphin GT;

Baltzer L,

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AAY78001 to AAY78100 represent peptides having sequences based on human lacroferin. The peptides are taken up in the intestine through binding to specific lactoferin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and Candida infections (such as urinary tract infections, collits, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives.

To discuss the perfect of the peptides are also fundated and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colltis; Candida infection; fungicidal;
bactericidal; preservative.
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               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                    Claim 22; Page 38; 102pp; English.
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98SE-0004614.
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections on a mucosal membrane), inflammations, colitis, and Candida infection on a mucosal in food stuffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Bven though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.
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                                                                                                                                                                                                                                                                                                                   100.0%; Score 71; DB 21; Length 12; 100.0%; Pred. No. 2.1e-05;
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98SE-0002562.
98SE-0004614.
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Best Local Similarity
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Best Local Similarity
Matches 11; Conserv
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17-JUL-1998;
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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumo
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                     ch 94.4%; Score 67; DB 21; Length 12; 1 Similarity 91.7%; Pred. No. 9.7e-05; 11; Conservative 1; Mismatches 0; Indels
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98SE-0002562.
98SE-0004614.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as urinary tract infearings and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-infearing and and anti-tumoural properties they cannot be used also used also because of high production costs. Therefore, provision of peptides because of high production costs. Therefore, provision of peptides because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
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           Length 12;
Score 67; DB 21; Length 12
Pred. No. 9.7e-05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    AAY78047 standard; Peptide; 12 AA.
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       94.48;
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AAY78037 standard; Peptide; 13
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                                                                                                                                                                                 food, infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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Pred. No. 9.7e-05;
1; Mismatches 0; Indels
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                                                                                                                                                Human lactoferrin derived peptide SEQ ID NO:84
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                                                                             AAY78084 standard, Peptide, 12 AA.
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91.78;
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98SE-0004614.
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Best Local Similarity 91.7°
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  1 CFQWKRNMRKVR 12
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17-JUL-1998;
29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food atuffs such as infant formula food. The peptides realso fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                           Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial; anti-tumour, urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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Pred. No. 0.00011;
1; Mismatches 0; Indels
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                                                          Human lactoferrin derived peptide SEQ ID NO:37
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       WO200001730-A1
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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25-APR-2000
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AAY78048
ID AAY78
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RESULT 7

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DAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment or through the circulation. A medicinal product of the peptide or fragment or invary tract infections. Collis, and candida infections (such as uncorrections and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Best Local Similarity 91.7%;
Matches 11; Conservative
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29-DEC-1998;
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Dolphin GT,

Baltzer L,

Mattsby-Baltzer I,

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the burdent of acceptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food sulfs such as infant formula food. The peptides can also be used as preservatives. The peptide and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.4%; Score 67; DB 21; Length 13; 91.7%; Pred. No. 0.00011; ...ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                      Dolphin GT
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                                                                                                                                                                                                                                      Baltzer L,
                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 74; 102pp; English.
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                                                                                                                                                                                                                                      Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                98SE-0002562.
98SE-0004614.
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hes 11; Conservative
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                                WO200001730-A1.
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29-DEC-1998;
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                                                                                                 06-JUL-1999;
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Synthetic.
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Matches
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0; Gaps

Score 67; DB 21; Length 13; Pred. No. 0.00011; 1; Mismatches 0; Indels

13 AA;

Homo sapiens

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Dolphin GT,

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as unionarian), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used as used as because of high production costs. Therefore, provision of peptides based on lactoferrin would contable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:50.
                                                                                                                                                                                                              Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78050 standard; Peptide; 14 AA
                                                                                                     Mattsby-Baltzer I,
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98SE-0002562.
98SE-0004614.
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91.7%;
                          98SE-0002562.
98SE-0004614.
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             98SE-0002441
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                                                                        (ASCI-) A+ SCI INVEST AB
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                                                                                                                                 WPI; 2000-147388/13
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Best Local Similarity
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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29-DEC-1998;
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Matches
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AAY78050
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as uncosal membrane), inflammations and/or tumours. The peptides can also be used in flood stuffs such as infant formula food. The peptides can also be used in flood stuffs such as infant formula food. The peptides can also be used and not actually and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                               New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 14;
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91.7%; Pred. No. 0.00011;
iive 1; Mismatches 0; Indels
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Baltzer L,
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                                                                                                                 Claim 15; Page 75; 102pp; English
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es 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            14 AA;
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29-DEC-1998;
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Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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0; Gaps

Score 67; DB 21; Length 14; Pred. No. 0.00011; L; Mismatches 0; Indels

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Claim 18; Page 75; 102pp; English

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                     Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                         food, infant formula, anti-inflammatory, anti-microbial, anti-tum
urinary tract infection, colitis, Candida infection, fungicidal,
bactericidal, preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
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                                                                                                                                                                            Human lactoferrin derived peptide SEQ ID NO:35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 69; 102pp; English.
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                                                 AAY78035 standard; Peptide; 15 AA.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity
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Synthetic.
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29-DEC-1998;
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Matches
         RESULT 14
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, collitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungatidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used alinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.4%; Score 67; DB 17; Length 15; 91.7%; Pred. No. 0.00012; ive 1; Mismatches 0; Indels
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heat-resistant and water-soluble
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Best Local Similarity 91.7%;
Matches 11; Conservative
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumourse. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                  Human lactoferrin derived peptide SEQ ID NO:62.
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25-APR-2000 (first entry)
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17-JUL-1998;
29-DEC-1998;
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Baltzer L,

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

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Search completed: February 21, 2003, 07:56:44 Job time : 29.093 secs

Query Match 94.4%; Score 67; DB 21; Length 15; Best Local Similarity 91.7%; Pred. No. 0.00012; Matches 11; Conservative 1; Mismatches 0; Indels

Sequence 15 AA;

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1 CFOWKRNIMRKVR 12

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APPLICANT: NAKASHIMA, HIDEKI

APPLICANT: NAKASHIMA, HIDEKI

APPLICANT: NAKASHIMA, SHIGERAL

APPLICANT: TANAKA, SHIGERAL

APPLICANT: TANAKA, SHUN'ICHI

APPLICANT: TANAKA, SHUN'ICHI

APPLICANT: TOSAKO, SHUN'ICHI

APPLICANT: TOSHIMA:

TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 8

CORRESSED: PATERY ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT

STREET: S3 STATE STREET

CITY: BOSTON

CITY: BOSTON
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NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: DEAD FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA::
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 93,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
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US-08-156-133-4
US-08-158-313-4
US-08-178-313-4
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US-09-265-577-2
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Patent No. 5565425
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MOLECULE TYPE: peptide
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STRANDEDNESS: si
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Sequence 1
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-31-984-25

US-09-508-734-6

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US-08-475-055-8
US-07-755-161A-3
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US-09-508-734-8
US-07-755-161A-8
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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71
1 CFQWKRNMRKVR 12
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jatabase :
                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
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18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NC
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-08-475-055-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                         Sequence B, Application US/08485948
; Sequence B, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
APPLICANT: HELEN VLASSARA
APPLICANT: ADRESSE:
ADDRESSEE: Aluber & Jackson
STREET: All Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                            Gaps
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                                                                          Score 67; DB 1; Length 18;
Pred. No. 9.9e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppd disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppd disk

COMPTING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,948

FILING DATE: 08/486,217

FILING DATE: APPLICATION DATA:

APPLICATION NUMBER: 08/418,642

FILING DATE: APRLICATION:

TELESCOMMUNICATION NUMBER: 947-1-008A

TELEPHONE: 201 487-5800

TELEPHONE: 201 487-5800

TELEFAN: 201 343-1684

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: AMINO SEQ ID NO: 8:

STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67; DB 2; Pred. No. 9.9e-05; 1; Mismatches 0
, OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                             Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO FRAGMENT TYPE: internal US-08-485-948-8
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CFOWORNMRKVR 12

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PSEQUENCE SERSIAN

APPLICANT: ULLS ONE WING

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CONNETS: Hadden wing

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CONNETS: HAD FOOD WING

MEDIUM TYPE: Flopy disk

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MEDIUM TYPE: Flopy disk

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MEDIUM TYPE: Flopy disk

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94.4%; Score 67;
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL INE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLORENY:
CLORENY:
CLORE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
CHROMOSOWE/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0. Thanh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/07755161A
Sequence 3, Application US/07755161A
Fatent No. 5304633
Fatent No. 5304633
Fatent No. 5304633
Fatent No. 5304633
Fatent INVENTION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Werderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
                                                                                                                                        COMPUTER READABLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION NUMBER: 08/486,948
FILING DATE:
APPLICATION NUMBER: 08/486,217
FILING DATE: APRIL 7, 1995
APPLICATION NUMBER: 08/48,642
FILING DATE: APRIL 7, 1995
APPLICATION NUMBER: 08/48,40.
FILING DATE: APPLICATION:
TELING DATE: APRIL 7, 1995
APPLICATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 201 487-500
TELEFRAM: 201 341-1684
TELEFRAM: 201 341-1684
TELEFRAM: 201 341-1684
TELEFRAM: ADDIT OF SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acid
STRANDEDNESS single
TYPE: APPLICATION: LP-C1, 8-25
HYPOTHETICAL: NO
ANTI-CENSER: NO
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
FRAGMENT TYPE:
JS-08-475-055-8
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LOCATION: 19
IDENTIFICATION WETHOD: 19
OTHER INFORMATION: () residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
NUTHOR INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "thiol group of
Cys residue at location 2 connected by disulfide bond with
thiol group of Cys residue at location 19"
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,1
FILING DATE: 1991095
CLASSIFICATION: 530
RIOR APPLICATION DATA:
APPLICATION NUMBER: 33,367
RIOR APPLICATION NUMBER:
FILING DATE: MATE: M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERRNCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELERAX: 202-371-8850
TERAX: 202-371-8850
TELERAX: 202-371-8850
TELERAX: 202-371-8850
TERAX: 202-371-8850
TELERAX: 202-371-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PUBLICATION DATE:
RELEYANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys re
OTHER INFORMATION: thiol
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: modified site LOCATION: 19
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Length 20;

DB 1;

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NAME / KEY: modified site
LOCATION: 19
LOCATION: 10
CHER INFORMATION: Cyg residue at location 19 connected by disulfide bond with
PUBLICATION INFORMATION: thiol group of Cyg residue at location 2"
AUTHORS:
                                                       //note= "thiol group of
Cys residue at location 2 connected by disulfide bond with
thiol group of Cys residue at location 19"
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APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NOSUCHI, WATARU
APPLICANT: MAKASHIMA, SHIGEAKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TAWASAKI, SOSHIHIRO
APPLICANT: TAWASAKI, YOSHIHIRO
APPLICANT: VAWASAKI, YOSHIHIRO
APPLICANT: UNJENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 94.4%; Score 67; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 0.00011; Matches 11; Conservative 1; Mismatches 0; Indels
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COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
TTING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSER: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSER: THIBEAULT
STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08204487; Patent No. 5565425
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFRENCK/POCKET NUMBER: FJN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32,503
                             IDENTIFICATION METHOD:
OTHER INFORMATION: /not
OTHER INFORMATION: Cys
OTHER INFORMATION: thic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOLUME:
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                                   Gaps
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Pred. No. 0.00011;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      Sequence 3, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:
GENERAL INFORMATION:
ABDERSAL INFORMATION:
AITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: Wenderoth, Lind & Ponack
STREET: BOS Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DisplayMite

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
TELEFAX: 202-371-8856
   91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: modified site
Best Local Similarity 91.7
Matches 11, Conservative
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DEVELOPMENTAL STAGE
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP_POSITION:
                                                                                          1 CFOWKRNMRKVR 12
                                                                                                                           2 CFQWQRNMRKVR 13
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CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                      US-07-891-174-3
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Gaps

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1 CFQWKRNMRKVR 12
                                                                                                                                                  2 CFQWQRNMRKVR 13
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Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                             RESULT 9
US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
            US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-08-381-984-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Manoru TOMITA et al.

APPLICANT: Manoru TOMITA et al.

TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES:
CORRESPONDENCES ADDRESS:
STRESSE: Wenderoth, Lind & Ponack
STREST: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUWRY: U.S.A.
ZIP: Z0005
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                       Query Match 94.4%; Score 67; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 0.00011; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
LOCATION:
LOCATION:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                           /note= "ANTIBACTERIAL PEPTIDE DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: LIBM COMPATIBLE
COMPUTER: LIBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: JULY 22, 1994
CLASSIFICATION 514
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-256-771-24
JS-08-256-771-24
Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION.
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
                                                                                                                                        MOLECULE TYPE: peptide
FRATURE: NAME/KEY: Peptide
LOCATION: 1..20
GTHER INFORMATION: OTHER INFORMATION: DERI
                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWKRINMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                             2 CFQWQRNMRKVR 13
                                                                                                                         linear
                                                                                                                         TOPOLOGY:
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TELEX:
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Sequence 25, Application US/08256771

Patent No. 555591

GENERAL INFORMATION:

APPLICANT: Mannor TOMITA et al.

TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING

TITLE OF INVENTION: PRODUCTS THEREWITH

NUMBER OF SEQUENCES: 3

CORRESPONDENCES: 4

ADDRESSE: Wenderoth, Lind & Ponack

STREET: Wenderoth, Lind & Ponack

CITY: Washington

STREET: D.C.

STREET: D.C.

STREET: 20005
                                                   Gaps
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US-08-256-771-25
    Score 67; DB 1; Length 20;
Pred. No. 0.00011;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.4%; Score 67; DB 1; Length 20; Ilarity 91.7%; Pred. No. 0.00011. Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible COMPUTER: IBM COMPUTER: BOSTWARE: MS-DOS SOFTWARE: Nordperfect 5.1
CURBENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: JALY 22, 1994 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Warren N. Cheek, Jr. REGISTRATION NUMBER: 33,36 REFERENCE/DOCKET NUMBER:
Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 20 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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MOLECULE TYPE: peptide
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LOCATION:
LOCATI
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CURRENT APPLICATION WUMBER: US/09/508,734
CURRENT FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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94.4%; Score 67; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                            805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWKRNMRKVR 12
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                                                                                                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: Sil
                                                                                                                                                                                            U.S.A.
                                                                                                                                                                                                                         20005
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                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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.. IDENTIFICATION METHOD:
.. OTHER INFORMATION: /note= "the specified peptide as well as
.. OTHER INFORMATION: peptides including the specified peptide as a fragment thereo
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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LOCATION:
LOCATION:
ODENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67; DB 1; Length 20;
Pred. No. 0.00011;
1; Mismatches 0; Indels
Sequence 24, Application US/08381984

Fater No. 5804555

GENERAL INFORMATION:
APPLICANT: Mamoru TOWITA et al.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wanderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: MOTOPETFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFCATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Pone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION MINBER:
REFFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
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US-08-381-984-25
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NAME/KEY:
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ORGANELLE:
INMEDIATE SOURCE:
ILIBRARY:
CLONE:
CLONE:
CHOMOSONE/SEGMENT:
MAP POSITION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                               ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFROM: 202-371-8856
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWKRNMRKVR 12
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Best Local Similarity
Matches 11; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CFQWQRNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
ANTT-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE:
CELL TYPE:
CELL LINE:
            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN:
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                                                                                                                                                                                                                  Gaps
                                                                                                                                                94.4%; Score 67; DB 4; Length 22; Illarity 91.7%; Pred. No. 0.00012; Conservative 1; Mismatches 0; Indels
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Sequence 10, Application US/07755161A

Sequence 10, Application US/07755161A

Patent No. 530463A

Patent No. 530463A

PAPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSES: Wenderoth, Lind & Ponack
STREET: 805 Fitteenth Street, N.W., #700

CITY: Washington

STATE: 0.C.

COUNTRY: U.S.A.

IP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500KD

COMPUTER: IBM Compatible

COMPUTER: STATE: D.C.

COMPUTER: DISKETE, MS-DOS

COMPUTER: DASSETEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA;
APPLICATION NUMBER;
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
COGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                                                                              1 CFQWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                             2 CFÓWORNMRKVR 13
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                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
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LENGTH: 24
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Gaps

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IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBBICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                  Query Match 94.4%; Score 67; DB 1; Length 25; Best Local Similarity 91.7%; Pred. No. 0.00013; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 21, 2003, 08:04:26 Job time: 8.93023 secs
                                                                                                                                                                                                                                   DOCUMENT NUMBER:
FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWKRNWRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CFOWORNMRKVR 15
                                                                                                                 TITLE:
JOURNAL:
                                                                                                                                                        /OLUME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-COUNTED TO SULTANTION:

Patent No. 5317084

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

Antimicrobial Peptides and an ITILE OF INVENTION:

Antimicrobial Agent
NUMBER OF SEQUENCE:

CORRESPONDENCE ADDRESS:

ADDRESSE:

Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STREET: BOC Fifteenth Street, N.W., #700

CITY: Washington

STREET: D.C.

COUNTER: IBM Compatible

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500Kb

COMPUTER: IBM Compatible

OPERATION STREET: US-DISKETE:

APPLICATION NUMBER: US/07/891,174

FILING DATE: DISPLAYMITE

FILING DATE: NUMBER: 33 367

REPERBONG-MONICATION NUMBER: 33 367

REPERBONG-MONICATION NUMBER: 33 367

TELEFROMMUTATION NUMBER: 33 367

TELEFROMMUTER: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX:
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: modified site LOCATION: 21
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Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
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APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
                                                      6000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
 TYPE: PRT
ORGANISM: HOMO SAPIENS
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RESULT 2
US-09-798-869-20
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 LENGTH: 15
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Matches
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Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appl
Sequence 2, Appli
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Sequence 1248, Ar
Sequence 119, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Appli
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                                                                                                     (without alignments)
54.162 Million cell updates/sec
                                                                                        February 21, 2003, 08:08:15 ; Search time 6.88372 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                       FULLISHER APPLICATIONS ANALY STATES AND STAT
            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-888-320-2
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US-09-925-301-1248
US-09-978-295A-119
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                                                                                                                                                                                                                                   156504 segs, 31069816 residues
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                                                                                                                                                                                                                                                                                                                                                                                Published Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                        US-09-743-107B-91
71
1 CFQWKRNMRKVR 12
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Query
Match Length DB
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Perfect score:
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Sequence 119, Appl
Sequence 14, Appl
Sequence 24, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 38, Appl
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Seguence 13026, A
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      Sequence 1
Sequence 1
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                 US-09-815-242-12129
US-09-815-242-13026
US-09-879-957-194
US-10-051-409-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION US/09798869
| Publication No. US20030022821A1
| GENERAL INFORMATION |
| APPLICANT: JOHN SIGURD SVENDEN |
| APPLICANT: GYSTEIN REKDAL |
| APPLICANT: ABLUDK SVEINBJ(RNSSON |
| APPLICANT: LARS VORLAND |
| TITLE OF INVENTION: BIOACTIVE PEPTIDES |
| FILE REFRERENCE: A34049-PCT-USA-A |
| CURRENT APPLICATION NUMBER: US/09/798,869 |
| CURRENT FILING DATE: 2001-02-7 |
| PRIOR APPLICATION NUMBER: GED818938.4 |
| PRIOR FILING DATE: 1998-08-21 |
| PRIOR FILING DATE: 1998-08-28 |
| NUMBER OF SEQ ID NOS: 30 |
| SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens ) OTHER INFORMATION: sequence) US-09-798-869-6
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Query Match 94.4%; Score 67; DB 9; Length 694; Best Local Similarity 91.7%; Pred. No. 0.0017; Matches 11; Conservative 1; Mismatches 0; Indels
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83.1%; Score 59; DB 9; Length 15;

Best Local Similarity 83.3%; Pred. No. 0.001;

Matches 10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                  WESOUT:

UG-798-869-6

Sequence 6, Application US/09798869

Publication No. US20030022821A1

SERNEAL INFORMATION:

APPLICANT: JOHN SIGURD SVENDEN

APPLICANT: LASS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: PCT/G899/02851

PRIOR PILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: GB9818938.4

PRIOR PLING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PRACES (for Windows Version 4.0)

SEQ ID NO 6

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-809-3

US-09-798-809-3

SQUENCE 3, Application US/09798869

PUBLICATION NO. US20030022821A1

GENERAL INFORMATION:

APPLICANT: OCHN SIGHEN SVENDEN

APPLICANT: TYSTEIN REKDAL

APPLICANT: BALDUR SVEINBJ(RNSON

APPLICANT: LARS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

TITLE OF INVENTION: BIOACTIVE PEPTIDES

TITLE OF INVENTION UNMER: US/09/798,869

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT PILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: GETGRB99/02851

PRIOR PILING DATE: 1998-08-31

PRIOR PILING DATE: 1998-08-31

PRIOR PILING DATE: 1998-08-31

PRIOR PILING DATE: 1998-08-38

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FREESED fOR Windows Version 4.0

SEQ ID NO 3

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.4%;
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                                                                                                                                     1 CFOWKRNMRKVR 12
                                                                                                                                                                     22 CFQWQRNMRKVR 33
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Best Local Similarity
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US-09-798-869-3
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Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
APPLICANT: OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67; DB 9; Length 25;
Pred. No. 8.2e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:

OCRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
ACCOBENT.
STREET:
A00 Seventh St. N.W.
CITY:
Washington D.C.
COUNTRY:
U.S.A.
ZIP:
ZOO04
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
CLASSITICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: PLAYER: 31,409
REGISTRATION NUMBER: 31,409
REGISTRATION NUMBER: 10505/P58185C
TELERCOMMUNICATION INFORMATION:
NAME: PLAYER: 31,409
REGISTRATION NUMBER: 31,409
REFERENCE FOOCKET NUMBER: 31,409
                            FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRACKEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 94.4%;
1 Similarity 91.7%;
11; Conservative 1
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amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-10-023-096-2
       LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo Sapiens
US-09-798-869-20
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Best Local Similarity
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54.5%; Pred. No. 1.3;
ive 2; Mismatches
                                                                                                                                                                                                                                                                            CURREAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANTON NOWBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NOWBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO SEQ ID NOS: 30
LENGTHS: 15
LENGTHS: 15
LENGTHS: 15
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEN REXDAL
APPLICANT: BALDUR SVEINBJ (RNSGON)
TITLE OF INVENTION: BIOACTURE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAELEST (1999-08-28)
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAELEST (1999-08-28)
SOFTWARE: FRAELEST (1998-08-28)
SOFTWARE: FRAELEST (1998-08-28)
SOFTWARE: PRESENTED (1990-08-28)
SOF
                                                                                                                                                                                                                            Sequence 4, Application US/09798869
Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.5-
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Matches 6, Conservative
          CFQWKRNMRKV 11
                                                                 CYCWOWRMRKL 13
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CRGANISM: MURINE
US-09-798-869-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-798-869-22
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      1; Indels
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                                                                                                                                                                                                                                         VESULE 6

US-098-869-23

Sequence 23, Application US/09798869

Publication No. US20030022821A1

SEGUENCEAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: LARS VORLAND
TILLE OF INVENTION: BIOACTIVE PEPTIDES
TILLE FEBERSENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798.869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31

PRIOR FILING DATE: 1998-08-31

PRIOR FILING DATE: 1098-08-38

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

STYPE: PRI
   3; Mismatches
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDEN
APPLICANT: VYSTEIN REXDAL
APPLICANT: BALDUR SVEINBJ (RNSON
APPLICANT: BALDUR SVEINBJ (RNSON
APPLICANT: BALDUR SVEINBJ (RNSON
TITLE OF INVENTION: BLOACITUR PEPTIDES
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PG899/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.0.
Conservative
                                                                 CFOWKRNMRKV 11
                                                                                                                        CYOWORRMRKL 13
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US-09-798-869-23
7;
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Matches
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Pred. No. 2.4;
4; Mismatches 2; Indels
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                                                                                                                                              US-00-798-869-29
Sequence 29, Application US/09798869
PUBLICATION NO. US20030022821A1
SERNEAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEIN RENDAL
PAPLICANT: BALDUR SYEINBAL
PAPLICANT: BALDUR SYEINBAL
PILLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TILE REPERRINCE: A34049-PCT-USA-A
CURRENT FILLING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR PELICATION NUMBER: PCT/GB99/02851
PRIOR PELICATION NUMBER: GB9818938.4
PRIOR PELICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PRACESED FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.5%;
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Best Local Similarity 45.5
Matches 5; Conservative
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1 CFOWKRINMRKV 11
                                    CYGWKRINKGV 58
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US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 29
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Pred. No. 29;
2; Mismatches 3; Indels
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Best Local Similarity 54.5
Matches 6; Conservative
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; ORGANISM: Mouse
US-09-796-753-26
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US-09-08-320-2.

Sequence 2, Application US/0988320

Publication No. US2003001309041

REMERAL INFORMATION:

APPLICANT: Barry III, Clifton E.

APPLICANT: Bekker, Inda Gail

APPLICANT: Bekker, Linda Gail

APPLICANT: Bek
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CRGANISM: Mycobacterium tuberculosis
OTHER INPORMATION: wild-type EtaA moncoxygenase (Rv3854c, EthA)
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO AL096701.14

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUE 1.00e-06
US-09-864-761-47985
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                                                          PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARR: Aniomax Sequence Listing Engine vers: 1.1
SEQ ID NO 47985
   APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.5
Best Local Similarity 83.3
Matches 5, Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 COKWPRRMRKM 263
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16 CFOWRR 21
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Sequence 47985, Application US/09864761
Sequence 47985, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Fank, David K.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Gene, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/203.66
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2000-01-0-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 9
Pred. No. 2.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                             APPLICANT: (YSTEIN REXOLAL APPLICANT: APPLICANT: (YSTEIN REXOLAL APPLICANT: EARS VORLAND
TILLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FSSESEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 15
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PILING DATE: 2001-01-30
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00668
                                                                                                     RESULT 13
JS-09-798-869-30
; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
                                                                                                                                                                                                                   Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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3 CFRWQWRMKKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFRWQWRMKKL 13
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ORGANISM: BOVINE
JS-09-798-869-30
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on:	, 07:48:01	; Search time 10.6047 Seconds (without alignments)
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71 1 CFQWKRNWRKVR 12 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

283224

Winimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73; \* 1: pir1: \* 2: pir2: \* 3: pir3: \* 4: pir4: \* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	errin	lactoferrin - goat		14		pyridoxamine 5'-ph	<u>-</u>	hypothetical prote	lactoferrin precur	hypothetical prote	-		hypothetical prote	cal		ribosomal protein	ribosomal protein	а	hypothetical prote	3-deoxy-manno-octu	probable monooxyge	diphosphate-fructo	26S proteasome SU	vif protein - simi	apolipoprotein B-1	hypothetical prote	T14P4.7 protein -	probable cytochrom	hypothetical prote
SUMMARIES	ΙD	TFHUL	JC2323	852107	T22597	H97451	AB2670	AG3441	AB0858	843	C84325	T08030	T18633	G86506	G72115	A48396	AH1301	AH1673	877802	AD2346	E64639	C70655	T01470	E90094	079	6095	T22879	8615	8451	2421
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hypothetical prote GTP-binding regula	hypothetical prote trichohyalin like	hypothetical prote hypothetical prote F1511.22 fimported	hypothetical prote 60S riboscmal prot	hypothetical prote pre-pilin leader p	33.3K hypothetical hypothetical	hypothetical prote MHC class I histoc	pectate lyase (EC
T17324 S52418	T28820 B85431	AC1714 AG1343 C96582	H81246 T00407	G98020 E82546	G86403 T16882	T29571 I37477	WZWCPC
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558 846	932 1432	0 0 0 0 0 4	131	283	23 E 0 84 0 9	361	374
52.1 1.1	52.1	50.7	50.7	50.7	50.7	50.7	50.7
37	37	9 9 9	36	36 36	36 36	36	36
30 31	33	8 8 8 8 8 8	1 K K	0.4 0.0	44 44 1. 2. 5. 4. 1.	4. 4. E. 4.	54.5

## ALIGNMENTS

				C,Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text_chang	C.Accession: G01394; S11228; $\overline{ ext{A}}$ 45401; S10324; S15853; S20 $\overline{ ext{8}}$ 41 $t$ ; $t$
	- human			21-Nov-	0324: S
	alidated]	c		revision	A45401: 83
	cursor [v	actoferri	ens (man)	#sequence	\$11228;
	errin pre	names: l	Iomo sapi	lar-1992	G01394;
TEHOL	lactotransferrin precursor [validated] - human	N, Alternate names: lactoferrin	C; Species: Homo sapiens (man)	1, Date: 31-N	Accession

RESULT 1

witch in the EMBL Data Library, March 1994

A;Reference number: G06820

A;Reference number: G06820

A;Reference number: G06820

A;Reteasion: G01394

A;Reteasion: G01394

A;Reference number: BmBL: U07643; NID: 9467236; PIDN: AAB60324.1; PID: 9467237

A;Reference: EMBL: U07643; NID: 9467236; PIDN: AAB60324.1; PID: 9467237

B;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Rose: 18, 5228, 1990

A;Reference number: S11228; MUID: 90384839; PMID: 2402455

A;Reference number: S11228, MUID: 90384839; PMID: 2402455

A;Reference number: EMBL: X53861; NID: 934415; PIDN: CAA37914.1; PID: 934416

A;Residues: 1-148, Tr. 150-422, Cr. 424-711 <REY>
A;Residues: 10-148, Tr. 150-422, Cr. 424-711 <REY>
A;Residues: 10-148, Tr. 150-422, Cr. 424-711 <REY>
A;Residues: 10-148, Tr. 150-422, Tr. 150 1ge 08-Dec-2000
S07160; A61169; A31000; S74

A,Molecule type: DNA
A,Residues: 1-15 <TEN>
A,ACTOSE-TEETENED DNA
A,Residues: 1-15 <TEN>
A,CTOSE-TEETENED DNA
A,CTOSE-TEETENED DNA
A,Experimental source: placenta
A,Note: sequence extracted from NCBI backbone (NCBIP:122202)
B,Powell, M.J.; Ogden, J.B.
Nucleic Acids Res. 19, 4013, 1990
A,Title: Nucleotide sequence of human lactoferrin cDNA.
A,Reference number: \$10324; MUID:90326549; PMID:2374734

A; Molecule type: mRNA A; Residues: 3-711 < POW>

A/Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Blocchen, J. 276, 349-355, 1991
A/Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A/Fitle: Expression of S15853, MUID:91264786; PMID:2049066
A/Reference number: 815853
A/Accession: 815853
A/Status: nucleic acid sequence not shown, not compared with conceptual translation

A; Molecule type: mRNA A; Residues: 20-31 <ST1>

A,Accession: S20841 A,Molecule type: protein A,Residues: 20-28,'X',30-31 <ST2>

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pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (st C;Species: Agrobacterium tumefaciens C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Dates: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman
                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S25107
Biochim. Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Accession: §52107; MUID:95127729; PMID:7827104
A;Accession: §52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-275 <WIL>
A;Residues: 1-275 <WIL>
A;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A;Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F53H4.4 - Caenorhabditis elegans
(S.psecies Caenorhabditis elegans
(S.psecies Caenorhabditis elegans
(S.pates: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
(S.Accession: T22597
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A,Introns: 67/1; 153/1
C,Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h similarity 72.7%; Pred. No. 2.2; Length 275; Similarity 72.7%; Pred. No. 2.2; 8; Conservative 1; Mismatches 2; Indels
                                 Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A,Molecule type: protein
A,Residues: 1-33 <QIA>
C;Superfamily: transferrin, transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Dobson, R. submitted to the EMBL Data Library, October 1996 submitted to the EMBL Data Library, October 1996 A;Reference number: 219587 A;Accession: T22597 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.2%; Score 47; DB 2; larity 54.5%; Pred. No. 0.12; Conservative 4; Mismatches
                                                                                                         3; Mismatches
                                     70.4%;
                                     Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                lactoferrin - sheep (fragment)
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                                                                                                                                                                                                                         CYQWQRRMRKL 48
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                                                                                                                                                                            1 CFQWKRNMRKV 11
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Matches 6; Conserv
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Matches 8; Conserv
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A, Map position: 3g21-3g23
C, Superfamily: transferrin repeat homology
C, Superfamily: transferrin repeat homology
C, Superfamily: transferrin #status predicted <81G>
E,1-19/Domain: signal sequence #status predicted <81G>
E,20-711/Product: lactotransferrin #status experimental <MAT>
F,20-711/Product: lactotransferrin prepat homology <TRH1>
F,21-36/Domain: transferrin repeat homology <TRH2>
F,30-65/39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status episte: carbohydrate (Asn) (covalent) #status experimental
F,368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Molecule type: mRNA
, Residuce: 3 -701, SWRVNV < PAN>
, Residuce: 3 -701, SWRVNV < PAN>
, Residuce: 3 -701, SWRVNV < PAN>
, Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
ur. J. Blochem: 145, 655-66, 1984
ur. J. Blochem: 145, 655-66, 1984
., Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
, Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nolecule type: protein
1, Molecule type: protein
1, Molecule type: protein
1, Molecules: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4, Mote: this is the final paper in a series
1, Mote: this is the final paper in a series
1, Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
1ur. J. Biochem. 241, 303-308, 1996
1ur. J. Biochem. 241, 303-308, 1996
1ur. J. Biochem. 241, 303-308, 1996
1ur. J. Accession: S74119; Mulb:97054624; PMID:8898921
                                                                              E
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A; Residues: 436-487, A', 489-711 <RAD>
A; Crose-references: EMBL:MNB4642; NID:9186815; PIDN:AAA86665.1; PID:9386855
R; Panella, T.O.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Tele: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A; Reference number: A61169; MUID:91235214; PMID:1674448
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Blochem, Blochkyr. Res. Commun. 203, 1324-1332, 1994
A; Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A; Reference number: JC2323; MUID:94380047; PMID:8093048
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human'myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Reference number: S07160
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A;Residues: 1-708 <LEP>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
F:359-696/Domain: transferrin repeat homology <TRH2>
F:359-696/Domain: transferrin repeat homology <TRH2>
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C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: JC2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: protein; RV, 26-27, XX', 30-32 <HOU>; Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>; Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
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Matches
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Species: Mus musculus (house mouse)
Spacies: Jo-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Space stons A28438 A41205
Pentecost, B.T.; Teng, C.T.
Parol. Chem. 252, 10134-10139, 1987
Spirite: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretizence number: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connexton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Akture 413, 848-852, 201,
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seron A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176
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typesidues 3-707 - PENA-
tytesidues 3-707 - PENA-
tytesidues 7-70 - PENA-
tytiu, Y.; Teng, C.T.
Tailo. Chem. 266, 21880-21885, 1991
Tytile: Characterization of estrogen responsive mouse lactoferrin promoter.
Tytile: Characterization of estrogen responsive mouse lactoferrin promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 2;
Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                           Score 41; DB 2;
Pred. No. 8.3;
1; Mismatches
                                    C,Genetics:
A,Gene: BMEL1517
A,Map position: I
C,Superfamily: pyridoxamine-phosphate oxidase
C,Keywords: oxidoreductase
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:Alternate names: lactotransferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.78;
                                                                                                                                                                                                                                               57.78;
58.38;
          A;Experimental source: strain 16M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 CFAWDMNKAKVR 361
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserva
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: AG3441
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
B; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
Mazur, M.; Golteman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:1175668
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Species: Agrobacterium tumefaciens
Jate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
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A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         er, E.W.
Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
Reference number: AB2577; PMID:11743193
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Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                               Residues: 1-206 <KUR>
Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSFDB:GN00169
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Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
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C;Superfamily: pyridoxamine-phosphate oxidase
                                                                                                                                                                                                                                                                                                                                                 1,Gene: AGR C 1391
1,Map position: circular chromosome
2,Superfamily: pyridoxamine-phosphate oxidase
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ilarity 58.3%;
Conservative
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Best Local Similarity
Matches 7; Conserv
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C)Accession: G86506
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kiehi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
Nucleic Acids Res. 28, 2311-2314, 2000
Nucleic Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: G86506
A;Accession: G86506
A;Accession: Lype: DNA
A;Residues: 1-759 <STO>
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
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A,Experimental source: strain J138
C;Genetics: A,Gene: CPj0126
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A;Molecule type: DNA
A;Residues: 1.447 - WNI2-
A;Cross-references: EMBL:Z68507; PIDN:CAA92831.1; GSPDB:GN00022; CESP:MI8.8
A;Experimental source: clone M18
                                                                                                                                                                                                                                                                                                                      hypothetical protein M18.8 - Caenorhabditis elegans
C.Species Caenorhabditis elegans
C.Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 29-0ct-1999
C.Accession: T18633; T23799
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Pred. No. 66;
2; Mismatches
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Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, February 1996 A;Reference number: Z18999 A;Accession: T18633
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submitted to the EMBL Data Library, January 1996
A;Reference number: Z19800
A;Accession: T23799
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A;Introns: 41/3; 137/1; 326/3; 434/2
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nilarity 66.7%;
Conservative
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1852 CFQWQSQLRYIQ 1863
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Matches 6; Conserved
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C;Accession: C84325
C;Accession: C84325
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S;
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld
Jung, K.H.; Alam, M.; Freitas, T.
Jung, K.H.; Alam, M.; Freitas, T.
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A64160; MUID:20504483; PMID:11016950
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C;Species: Chlamydomonas reinhardtii
C;Species: 21-May-1999 #text_change 02-Feb-2001
C;Dates: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Accession: T08001
E;Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Titlell Sci. 107, 635-644, 1994
A;Titlell Sci. 107, 635-644, 1994
A;Titlell Sci. 216302; MUD:94274778; PMID:8006077
A;Accession: T08030
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A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 366/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866/4; 3866
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-584 <STO>
A; Ccoss-references: GB: AE004437; NID: g10581192; PIDN: AAG19967.1; GSPDB: GN00138
C; Genetics:
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;Molecule type: DNA;
;Mesidue: 1-4568 -MID:
;CROSG-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215;
;Sxperimental source: strain 21gr
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F;20-707/Product: lactotransferrin #status predicted <MAT> .
F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                           Query Match 57.7%; Score 41; DB 1; Length 707; Best Local Similarity 54.5%; Pred. No. 28; Ansatches 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 2; Length 584;
Pred. No. 34;
4; Mismatches 3; Indels
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Pred. No. 2.6e+02;
4; Mismatches 3; Indels
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Best Local Similarity 41.7%;
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ibosomal protein L28 - Bacillus stearothermophilus
);Species: Bacillus stearothermophilus
);Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 21-Aug-1998
);Accession: A48396
);Kruft, V.; Kapp, U.; Wittmann-Liebold, B.
icohimie 73, 855-860, 1991
icohimie 73, 855-860, 1991
i;Title: Characterization and primary structure of proteins L28, L33 and L34 from Bacill
i;Reference number: A48396; WUID:92075758; PMID:1742360
ypochetical protein CP0646 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR Species: Chlamydophila pneumoniae, Chlamydia pneumoniae, pate: 23.Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
Accession: G72115; F81554
*Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Ature Genet. 21, 385-389, 1999
*Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
*Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                               Status: preliminary
"Molecule type: DNA"
"Presidues: 1-759 cARNA"
"Presidues: 1-759 cARNA"
"Cross-references: GB:AE001599; GB:AE001363; NID:g4376387; PIDN:AAD18279.1; PID:g437639
"Experimental source: strain CWL029
"Experimental source: strain CWL029
"Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, Rr; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Ncleic Acids Res. 28, 1397-1406, 2000
"Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39."
"Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,Molecule type: DNA
,Residues: 1-759 <REA>
,Cross-references: GB:AE002222; GB:AE002161; NID:g7189553; PIDN:AAF38461.1; PID:g718956
,Experimental source: strain AR39, HL cells
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A,Molecule type: protein
A,Residues: 1-60 <KRUS
A,Note: sequence extracted from NCBI backbone (NCBIP:69662)
C;Superfamily: Escherichia coli ribosomal protein L28
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
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drosophila

P35649 eikenella c P58306 thermoplasm Q991c6 homo sapien Q99up4 staphylococ P29328 ovis aries Q10353 schizosacch P4348 mus musculu P19506 simian immu Q55185 synechocyst

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Cho Y.Y.;
Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferroxin A;
Lattoferroxin B; Lactoferroxin C].
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

TISSUE=Mammary gland;

MEDLINE=90384839; PubMed=2402455;

Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;

"Complere nucleotide sequence of human mammary gland lactoferrin.";

Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Nammary gland;
Liang O., Jimenorz-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Bone marrow;
Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region DNA
                                                                                                                                                                                         TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16785; Q16789; O00756; Q9H1Z3; Q96KZ4;
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TISSUE-Mammary gland;
THSSUE-Mammary gland;
THORD H., Chen X., Huan L.;
"CDNA Cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Straubberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
[8]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences.";
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                        ALIGNMENTS
088A DROME
SYH CHLMU
MSSI SCHPO
YHAZ EIYCO
PPCK THEVO
PDII HUWAN
RL28 STAAM
                                                                             RL24_SCHPO
TNF4_MOUSE
VIF_SIVSP
Y495_SYNY3
 4401
4428
4428
6633
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1192
1192
214
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TISSUE=Mammary gland;
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TISSUE=Prostate;
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                                                                February 21, 2003, 07:28:06; Search time 5.2093 Seconds (without alignments) 95.544 Million cell updates/sec
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         GenCore version 5.1,3
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                             112892 seqs, 41476328 residues
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HV2ST
BACSU
BACAM
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NLA DROME
RL2@ BACST
RL2@_LISMO
RPOB_LIBAF
Y125_MYCCA
VIF_SIVS4
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CAX1 ARATH
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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoi L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgarald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L., to the EMBL/GenBank/DDBJ databases.
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MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                             "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
Biochim. Biophys. Acta 670:243-254 (1981).
                                                                                                                                                                                                                                                                                  PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE-82046817; PubMed=6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=82262043; PubMed=7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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MEDLINDE=97156796; Pubmed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedle J.W.,
Baker E.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-253-->methionine mutant.";
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MEDLINE-88001031; PubMed-3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library an expression of mak during normal and leukemic myelopoiesis.";
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Legrand D., Spik G., Montreull J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'An 88 amino acid long C-terminal sequence of human
                TISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
Powell M.J., Ogden J.E.,
NNUCLOCITA Sequence of human lactoferrin CDNA.";
Nucleic Acids Res. 18:4013-4013(1990).
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MEDLINE=99190892; Pubmed=10089347;
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SEQUENCE OF 237-711 FROM N.A.
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  SEQUENCE OF 3-711 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                          Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
A Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
B. Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
B. Heitmancik J.P., Teng C.T.;
T. Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene..!,
Mol. Vision 4:31-32(1998).
I. FUNCTION: TRANSFERINS ARE IRON BINDING TRANSFORT PROTEINS WHICH
CAN BIND TWO ATOMS OF ERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
C. PUNCTION: LACTOFERROXIN A, BAND C HANZ OPIDID ANTAGONIST
C. PUNCTION: LACTOFERROXIN A, SOMEWHAT HICHER DEGREES OF PREFERENCE
C. LACTOFERROXIN B AND C HANS SOMEWHAT HICHER DEGREES OF PREFERENCE
C. CANDERSONIST THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                    CHRACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Ito K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived from human lactoferrin.";
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                  MEDIINE=99192677; PubMed=10089508; Jameson G.B., Thomas D.H., Baker B.N.; Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker B.N.; Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
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-i-DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i-SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                     X-RAY CRYSTALLOGRAPHY (2,0 ANGSTROMS)
                                                                                                                                                                                                                                                                                               Agric. Biol. Chem. 54:1803-1810(1990)
                                                     Acta Crystallogr. D 55:403-407(1999).
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EMBL; U07643; AAB60324.1; -.
EMBL; M93150; AAA36159.1; -.
EMBL; M83205; AAA59511.1; -.
EMBL; M83205; AAA58656.1; -.
EMBL; M18642; AAA86665.1; -.
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X52941; CAA37116.1;
U95626; AAB57795.1;
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Submitted (Unv.199) to the RMBL/Genbank/DDBJ databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ADOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
-!- FUNCTION: TRANSFERRING PERRIC IRON IN ASSOCIATION WITH THE BINDING
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                  Gaps
                                                                                                                                                                                                                Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Cameluae, Camelus
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Somal; STRAIN-Somal; TISSUE-Lactating mammary gland; Kappeler S.R., Ackermann M., Farah Z., Puhan Z.; "Sequence analysis of camel (Camelus dromedarius) lactoferrin."; Int. Dairy J. 9:481-486(1999).
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InterPro; IRRO1156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTE; PR00425; TRANSFERRIN.
SWART; SM00042; TRER; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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            Length 711;
         Score 67; DB 1; Length 711
Pred. No. 0.0002;
1; Mismatches 0; Indels
                                                                                                                                  TRFL_CAMDR STANDARD; PRT; 708 AA. O9TUMO; OSMZSS; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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EMBL; AF165879; AAF82241.1; -.
HSSP; O77811; 1B1X.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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MEDLINE-94380047; Pubmed=8093048;
MEDLINE-94380047; Pubmed=8093048;
MEDLINE-94380047; Pubmed=8093048;
MEDLINE-94380047; Pubmed=8093048;
"Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 syntemy group.";
Biochem. Biophys. Res. Commun. 203:1324-1332(1);
FINCTION: TRANSFERRINS ARE IRON BINDING TRANSFORT PROTEINS WHICH CAN BIND, USUALLY BICARBONATE.
OF AN ANION, USUALLY BICARBONATE.
-1- SUBGUILT: MONOMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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AC G29477; Q29479;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin);
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STANDARD;
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                                                        TRFL HORSE
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                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Bwlopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8D-sib.ch).
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                                                                                                                                               EMBL; U53857; AAA97958.1; -.
BRBL; X78902; CAA55517.1; -.
HSSP; O77698; ICE2.
InterPro; IPR001156; Transferrin.
Pfam; PF00402; TRANSFERRIN.
PRINTS; PR00422; TRANSFERRIN.
SMART; SMO0094; TR PER, 2.
PROSTIE; PS00206; TRANSFERRIN.
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L -> R (IN REF. 2).
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D -> G (IN REF. 2).
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IRON 1 (BY SIMILARITY).

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IRON 1 (BY SIMILARITY).

IRON 2 (BY SIMILARITY).

ANION (BY SIMILARITY).

ALINKED (GLUNAC. ..) (

N-LINKED (GLUNAC. ..) (
DOMAIN: COMPOSED OF TWO HOMOLOGGUS DOMAINS. SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN.
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1 CFQWKRNMRKV 11 |:||:||: 38 CYQWQRRMRKL 48

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THE CONTRICTORS STANDARD; PRT; 695 AA.

TO TATALLASO (Rel. 18, Created)

DT 11-TUT-199 (Rel. 199)

DE 11-TUT-199 (Rel. 1
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                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=M84 / JCK 11007;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
Chen Y., Xue Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Yu Z., Yang H.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
-1- SIMILARITY: BELONGS TO THE L28P PAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                (POTENTIAL)
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                       1; Indels
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Pred. No. 0.69;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L28.
RPMB OR TTE1495.
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4; Mismatches
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15-JUN-2002 (Rel. 41, Last seq.
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                             75991 MW;
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Local Similarity 70.0%;
les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Best Local Similarity 58.3
Matches 7; Conservative
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695 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu Y., Teng C.T.,
"Characterization of estrogen-responsive mouse lactoferrin promoter.",
"Characterization of estrogen-responsive mouse lactoferrin promoter.",
"J. Biol. Chem. 266:21885(1991).
-!- FUNCTION: TRANSTERRING ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USTALLY BICARBONATE.
-!- SUBDIT: MONOWER.
-!- SUBDIT: MONOMER LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pentecost B.T., Teng C.T., ^{\prime}
                                                                                                                                                                                                                                        Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00205; TRANSFERRIN_1; 1.
PROSITE; PS00206; TRANSFERRIN_3; 2.
PROSITE; PS00207; TRANSFERRIN_3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                P08071; P70690; Q61799; Q922P2;
01-MG-1988 (Rel. 08, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annocation update)
Lactotransferrin precursor (Lactoferrin)
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LACTOTRANSFERRIN.
1.
                             707 AA.
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                                PRT;
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EMBL; M74778; AAA3427.1; --
PIR; A28438; A28438.
HSSP; P02788; LCB6.
MGD; MGI:96837; Ltf.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
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MEDLINE=87280033; PubMed=3611056;
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MEDLINE=92042099; PubMed=1939212;
STANDARD;
0922P2;
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EMBL; D88510; BAA13633.1; -.
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                             TRFL MOUSE
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Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Perrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                                       COLLED COIL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COIL (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
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InterPro; IPR004273; Dynain heavy.
Pfam; PP03028; Dynain heavy. 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 4568;
       -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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Pred. No. 92;
4; Mismatches
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Matches 5; Conservative
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Cell SCI. 107-1635-644(1994).

- Cell SCI. 107-1635-644(1994).

- PUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND PLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.

DYNEIN HAS ATTRAGE ACTIVITY.

- SUBDILI: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANION (POTENTIAL).
ANION (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
MR -> 1QG (IN REF. 1).
MR -> Q (IN REF. 2).
M -> L (IN REF. 2).
S -> T (IN REF. 2).
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A -> D (IN REF. 2).
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagt annotation update)
Dynein beta chain, flagellar outer arm.
CDA4 OR ODA-4 OR SUPI
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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F26AE0340A4C19A8 CRC64;
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Pred. No. 8.7;
2; Mismatches
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BY SIMILARITY.
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delicher A., Deng Z., Mays A.D., Dew I. Dietz S.M., Bodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K.J., Evangelista C.C., Ferriaz C., Ferriazs S., Felsischmann W., RA Poalreilan A.B., Garrell J.H., Galbart W.M., Glasser K., Adong F., Gorzell J.H., Gu Z., Galbart W.M., Glasser K., Adong F., Gorzell J.H., Gu Z., Gaun P., Harris M., Harris N.L., Harnandez J.R., Houck J., Harris M., Adlanh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Maltshia B., McIntcesh T.C., McLecd M.P., Mopherson D., Mattei B., McIntcesh T.C., McLecd M.P., Mosherson D., Mattei B., McIntcesh T.C., McLecd M.P., Mosherson D., And Jalazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G., Reinert K., Remington K.A., Murphy L., Murshy D., Puri V., Resee M.G., Shen B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shur S., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Alber R.A., Where E.W., Rubin G. M., Venter E. Sinner S., Zho X., Manghas R., Shing S., Anders E. M., Rubin G. M., Weissenbach J., Shur S., Engleron M., Shong W., Zhou X., Zhu S., Zho X., Smith H.O., Alber R.A., Whore E.W., Rubin G. M., Venter J.C., Scheng L., Shing S., Shong S., Yao Q.A., Thengence of Drosophila melanogaster.", Schur S., Smith H.O., Leinere L. FIRWATTON. PROTINTER P. C. FIRMATON. PRINTIPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kruft V., Kapp U., Wittmann-Liebold B.;
"Characterization and primary structure of proteins L28, L33 and L34
from Bacillus stearothermophilus ribosomes.";
Blochimie 73:855-860(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000).
-!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
-!- SIMILARITY: BELONGS TO THE DSCRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 54.9%; Score 39; DB 1; Length 292; Best Local Similarity 54.5%; Pred. No. 7.9; Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIZE BACST STANDARD; PRT; 60 AA. P23374; 01-NOV-1991 (Rel. 20, Created) 1-NOV-1991 (Rel. 20, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 50S ribosomal protein L28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus stearothermophilus.
Bacteria, Firmicutes, Bacillales, Geobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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MEDLINE-92075758; PubMed=1742360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF147700; AAD33987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0026629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 FOWLRSFRRLR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FOWKRINMRKVR 12
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         $$$$$$$$$$$$$$$$$$$$$$$$$$$$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glaser P., Frangel E., Buchrieber C., Rusniok C., Amend A., Baquero F., Barche P., Chartaborty T., Charbit A., Checuani F., Couve B., de Daruvar A., Dehoux P., Converbit A., Checuani F., Couve B., de Daruvar A., Dehoux P., Domann B., Dominguez-Bernal G., Duchaud B., Durant L., Dussurget O., Entian K.-D., Febin H., Garcia-del Portillo F., Garrido P., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurspkat G., Matcurnam A., Mata Vicente J., Ny E., Nedjari H., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Purcell R., Varquez-Boland J.-A., Voss H., Wehland J., Cossart P., Corparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
-!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE 128P FAMILY OF RIBOSOMAL PROTEINS
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                                                                                                                                                                                                                                                                        Score 38; DB 1; Length 60;
Pred. No. 2:3;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=L.monocytogenes, and L.innocua;
STRAIN=EGD-e / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.5%; Score 38; DB 1; Length 62; 66.7%; Pred. No. 2.3; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                             60 AA; 6810 MW; 2AD9161CD60E82F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA43DE039213C562 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TS-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L28.
RPMB OR LMO1816 OR LINI930.
                   PIR; A48336; A48396.
InterPro; IRF001383; Ribosomal L28.
Fam; PFC0830; Ribosomal L28, T.
TIGRFAMS; TIGRO0009; L28; 1.
Ribosomal protein.
INIT MET
SEQUENCE 60 AA; 6810 MW; 2AD9161C
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SEQUENCE 62 AA; 6991 MW; AA43DE03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21537279; PubMed=11679669;
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EMBL; AL596170; CAC97160.1; -.
                                                                                                                                                                                                                                                                        53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeria monocytogenes, and
                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    4 WKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                        27 WKANLQKVR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria innocua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL28 LISMO
Q92AJ2;
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RL28_LISMO
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EMBL; X14307; CAA32484.1; -.
PIR; SO7989; SO7989.
HIV; X14307; VIFSSWMH4.
InterPro; IPROC0475; Viral_infect.
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Les 7; Conservative
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         NCBI_TaxID=2095;
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VIF.SIVS4
VIF.SIVS4
VIF.SIVS4
DT 01-0C
DT 01-0C
DT 01-NC
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         STAR REPRESENT TO THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Nelspruit,
Planet P., Jagoueix S., Bove J.M., Garnier M.;
"Detection and characterization of the African Cirrus Greening
Liberobacter by amplification, cloning and sequencing of the rplKAUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {RNA}(N).
SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                             Exertuacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Transcription; DNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
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Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
Entomoplasmataceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                        146 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001572; RNA_pol_B.
Pfam; PF00562; RNA_pol_B; 1.
PROSITE; PS01166; RNA_FOL_BETA; PARTIAL.
                                                                                                                                                                                                                        PRT;
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Y125 MYCCA
ID Y125 MYCCA
ID Y125 MYCCA
STANDARD; PRT;
AC P53661;
DT 01-0CT-1996 (Rel. 34, Last sequence
DT 01-0CT-1996 (Rel. 34, Last sequence
DT 01-0CT-1996 (Rel. 34, Last sequence
DT MYCOplagma capticolum.
OS MYCOplagma capticolum.
OC Bacteria; Firmicutes; Mollicutes; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U09675; AAA19557.1; -
                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWKRNMRK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                    29 WKANLQKVR 37
4 WKRNMRKVR 12
                                                                                                                                                                                                                     RPOB LIBAF
P41187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
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SECUENCE FROM N.A.
SECUENCE FROM N.A.
STRAIR=ATCC 27343 / KID;
MEDLINE=SOC59641; PubMed=4476192;
BOTK P., Ouzounis C., Casari G., Schneider R., Sander C.,
BOTA M., Gillevet W., Gillevet P.M.;
"Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology.";
Mol. Microbiol. 16:955-967 (1995).
-! SIMILARITY: BELONGS TO THE COF/YEHA/XIDA/YIGL (B.COLI) / YCSE/YXEH (B.SUBTILIS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "An African primate lentivirus (SIVsm) closely related to HIV-2.";
Nature 339:389-392(1989).
-!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=89262053; PubMed=2786147;
Hirsch V.M., Olmstead R.A., Murphey-Corb M., Purcell R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 AA; 30425 MW; D5912DD5B39A8451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Virion infectivity factor (SOR protein) (Q protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 AA
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InterPro; IPR001454; Hignase/hydrlase.
InterPro; IPR00150; Hydrothet_cof.
Fram; PF00702; Hydrolase; I.
PROSITE; PS01229; COF_1; 1.
Hypothetical protein.
NON TER 267 25, 267
SEQÜENCE 267 AA; 30425 MW; D5912DD5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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CARBOHYD
DISULFID
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DOMAIN
TRANSMEM
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                                                                                         Gaps
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1834 HUMAN STANDARD, PRT, 365 AA.
P30453; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34 (A-10) alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: FAD (POTENTIAL)
-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
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                                                                Query Match
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 52.1%; Score 37; DB 1; Length 783; Local Similarity 50.0%; Pred. No. 50; to Conservative 2; Mismatches 4: ThAster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, 235602; CAA84671.2; -..
wormbep; R13G10.2; CESCOR8.
InterPro; IRR002937; Amino oxidase.
Pfam; PF01593; Amino oxidase; 1.
Hypochetical protein; Oxidoreductase; Flavoprotein; FAD. NP BIND
NP BIND
SEQUENCE 783 AA; 88799 MW; BD087E96464DC908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       Durbin R.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                             Gardner A.E.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                             214 AA; 25140 MW; 9BCE884EC454BF3D CRC64;
                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein R13G10.2 in chromosome III.
R13G10.2.
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRICNINFFCT.
ProDom; PD000063; Viral_infect; 1.
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 CIDWGRDDRKVK 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                 170 OWRRINKK 177
                                                                                                            3 OWKRINMRK 10
                                                                                                                                                                                       CAEEL
                                                                                                                                                                                                                                                                                                                                                                              REVISIONS.
                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                RESULT 14
YNR2_CAEEL
ID YNR2_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      du Toit E.D., Parham P.;
"Structural diversity in the HLA-A10 family of alleles: correlations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (A*3401/A*3402).

MEDLINE=99056508; PubMed=1431115;

Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,

Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,

Martell R.W., du Toit E.D., Parham P.;

Joisinctive HiA-A,B antigens of black populations formed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93235211; PubMed-8475492;
Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401 (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
                           Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Antigens 41:72-80(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal; Polymorphism.
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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/FIId=VAR 004379.
K -> N (IN A*3402).
/FIId=VAR 004380.
R -> I (IN A*3402).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interallelic conversion.";
J. Immunol. 149:3411-3415(1992).
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EMBL; X61705; CAA43873.1; -...
PIR; S16771; S1677.
HSSP; O19673; 11458.
MIN; 142800; -...
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
Pfam; PPR00129; MHC_1; Pfam; PPR00129; MHC_1; I...
Pfam; PPR00129; MHC_1; I...
PROSITE; PR00290; IG_MHC; I...
RMART; SM00407; IGGL; I...
PROSITE; PS00290; IG_MHC; I...
RGGAL Transmembrane; Glycoprot SGGAL I...
SGGAL Transmembrane; Glycoprot SGGAL I...
SGGAL Transmembrane; Glycoprot SGGAL I...
SGGAL TRANSMEMBRANE I...
SAGGAL TRANSMEMBRANE I...
SAGGAL TRANSMEMBRANE I...
SAGGAL I...
SAGGAL TRANSMEMBRANE I...
SAGGAL II...
SAGGAL
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HLA-A OR HLAA.
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				RC64;
P -> S (IN A*3402).	/FIIG=VAK 004382. Q -> R (IN A*3402).	/FIIG=VAK 004383. W -> L (IN A*3402).	FIIG=VAR 004384. L -> I (IN A*3402).	/FIId=VAR 004385, 365 AA; 41055 MW; 063BF63EGEGED1F6 CRC64;
129	138	180	312	41055 N
129	138	180	312	365 AA;
VARIANT	VARIANT	VARIANT	VARIANT	SEQUENCE
F. E	1 <b>E</b> E	4 [4 [	- [- 4 [4	SQ.

Query Match
 50.7%;
 Score 36;
 DB 1;
 Length 365;

 Best Local Similarity
 66.7%;
 Pred. No. 34;
 Mismatches
 2;
 Indels

 Matches
 6;
 Conservative
 1;
 Mismatches
 2;
 Indels

 / HENDRIKK
 1
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 4
 MISMARK
 92

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 93
 94
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0; Gaps

Search completed: February 21, 2003, 07:51:38 Job time : 6.2093 secs

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Q9jjzs mus musculu
Q22955 chlamydia p
Q22955 chlamydia p
Q82951 encephalito
Q8873 encephalito
Q9876 encephalito
O9084 human immun
Q7785 human immun
Q7785 human immun
Q7785 human immun
Q98765 cryza sativ
Q8747 salmonella
Q8774 salmonella
Q8774 salmonella
Q8774 salmonella
Q8779 mus mesculu
Q8780 cryza sativ
Q25611 helicobacte
Q2518 oryza sativ
Q2518 oryza sativ
Q9718 helicobacteri
Q9718 crea ariet
Q9718 crea ariet
Q9410 cryza sativ
Q8487 ca mays (m
Q8437 arabidopsis
Q9410 ttv-like mi
Q9415 drosophia
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    017549 caenorhabdi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.3%; Score 62; DB 4; Length 711; 90.9%; Pred. No. 0.0074; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022347; AAH22347.1; -.
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                       Q9SML2
Q68541
Q8YP77
Q8TAX2
Q9F7Y4
017549
Q9JJZS
Q9Z955
Q6Z582
Q8SRG3
Q8SQ16
090884
Q77855
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Q9QU30
Q9W1D5
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081653
Q9ZTP0
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Q8S487
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Q9XFX1
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
    Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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   Lactotransferrin.
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   Q8TCD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UCY5
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09UCYS
1D 09UCY
AC 09UCY
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DT 01-M
DF 01-M
OB- Lactc
OS Home
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Q8TCD2
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Q9uvy5 homo sapien
Q9tr90 caenorhabdi
Q8790 caenorhabdi
Q8790 thermoanaer
Q9860 thizobium 1
Q80ths rizobium 1
Q80ths rizobium m
Q87ths rizobium m
Q87ths rizobium m
Q87ths rizobium m
Q97ths rizobium m
Q97ths desamum ind
Q97m1 homo sapien
Q97m1 homo sapien
Q97m21 homo sapien
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114.078 Million cell updates/sec
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                                                                                             February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
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                                                                                                                                                                                                                                                                                   671580
             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Q9UCY5
Q9UCY5
Q93780
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Q98R9U1
Q9CKR3
Q9ZKR3
Q9ZKR3
Q9ZKR3
Q9ZKR3
Q9ZKR3
Q9ZKR3
Q9ZKR3
Q9ZKR3
Q9ZKR1
Q9GR3
Q9GR3
Q9GR3
Q9HPA3
Q9HP
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sp_phage:*
sp_plant:*
sp_roden:*
sp_virus:*
sp_virus:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
sp_mhc:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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4aximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Bacteria, Firmicutes, Bacillus/Clostridium group, Clostridia, Thermoanaerobacteriales, Thermoanaerobacteriaces, Thermoanaerobacteriaces, Thermoanaerobacter. NCBI TaxID=119072;
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SEQUENCE FROM N.A.

MEDLINE=21992816, PubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
Genome Reg. 12:689-700(2002).

Genome Reg. 12:689-700(2002).
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Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Watshida Y.; Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
                                                                 Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41, DB 16, Length 62, Pred. No. 3.6, 2, Mismatches 1; Indels
                                                                                                                                                                                             h Similarity 72.7%; Score 45; DB 5; Length 275; Similarity 72.7%; Pred. No. 3.1; 8; Conservative 1; Mismatches 2; Indels
                                                                                      investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281082 CAB03137.1; ..
SEQUENCE 275 AA, 31716 MW, 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-0cT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Pyridoxamine 5'-phosphate oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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70.0%;
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal protein L28.
RPMB OR TTE1495.
                                                                                                                                                                                                                                                                                                                  262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                        2 FOWKRINMRKVR 12
                                                                                                                                                                                                                     Local Similarity
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SEQUENCE 62 AA;
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Q8R9U1;
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                         "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries (Sheep).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae; Caprinae; Ovis.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                    ch 81.7%; Score 58; DB 4; Length 38; 1 Similarity 90.9%; Pred. No. 0.0019; 10; Conservative 1; Mismatches 0; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
[2]
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                                                                                                                                                                                                           InterPro; IPRO01156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                              seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995)
HSSP; P02788; 1BKA.
                                                                                 MEDLINE=96081613; PubMed=8551695;
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Matches 10; Conser
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                                                            SEQUENCE FROM N.A.
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F53H4.4.
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                     NCBI_TaxID=9606;
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RESULT 3 Q9TR80

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1 CFOWKRNMRKVR 12
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Best Local Similarity
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SEQUENCE FROM N.A.
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Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21608550; PubMed=11743193; Works D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Mond G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McCelland E., Palmieri A., Cardon G., Raymond C., Rouse G., Samphimmachak C., Wu Z., Romero P., Gordon D., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.; Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.; The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Gurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
"Genome Bequence of the plant pathogen and biotechnology agent
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-UUN-2002 (TYEMBLrel. 21, Created)
01-UUN-2002 (TYEMBLrel. 21, Last sequence update)
01-UUN-2002 (TYEMBLrel. 21, Last annotation update)
Pyridoxamine 5. -phosphate oxidase.
PDXH OR ATUO760 OR AGR C_1381.
Agrobacterium tunefaciene (strain C58 / ATCC 33970).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                     57.7%; Score 41; DB 16; Length 205; 58.3%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.7%; Score 41; DB 16; Length 206; ilarity 58.3%; Pred. No. 12; Conservative 1; Mismatches 4; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                 205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                DNA Res. 7:331-338(2000).
EMBL, AP003011, BAB53553.1; -.
EMBL, AP003011, BAB53553.1; -.
EMBL, PF01243, Pyridox oxidase.
Fram, PF01243, Pyridox oxidase, 1.
ProDom, PD006312; Pyridox oxidase, 1.
TIGNFAMS; TIGNF00558; pdxH; 1.
PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
COMDIETE protecome.
SEQUENCE 205 AA; 23300 WW, OBADE4CD:
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                                                                                                                                                                                                                                                                                                                                       Query Match
Query Match
Best Local Similarity 58.33,
7; Conservative
                                                                                  Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
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Matches 7; Conserv
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SEQUENCE 206 AA
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QBUHC2,
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A Boiderard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S.,
Boddrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Goffeau A., Wahler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizoblum mellioti strain 1021."
I Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
R EMBL, AL591785; CAC4547.1;
R InterPro; IPR006659; Pyridox oxidase.
R Probon, PD066312; Pyridox oxidase.
R Probon, PD066312; Pyridox oxidase; 1.
R PROSITE; PS01064; PYRIDOX_OXIDASE; UNKNOWN_1.
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STRAIN=16M / ATCC 23456 / BIOTYPE 1;
STRAIN=20020109; DubNed=11756689;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.,
The genome sequence of the facultative intracellular pathogen
                                        Variable (Tremble). 19, Created)
01-DEC-2001 (Tremble). 19, Last sequence update)
01-DTM-2002 (Tremble). 19, Last sequence update)
01-DTM-2002 (Tremble). 21, Last annotation update)
01-DTM-2002 (Tremble). 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
(EC 1.4.3.5).
PDXH OR R00895 OR SMC00069.
Rhizobium mellioti (Sinorhizobium mellioti).
Rhizobiaceae; Sinorhizobium.
Rhizobiaceae; Sinorhizobium.
NCBI _TaxID=382;
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Brucellaceae; Brucella.
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase, Complete Proteome. -
SEQUENCE 206 AA, 23900 MW, A2DB74229DACA97A CRC64;
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58.3%; Pred. No. 12;
iive 1; Mismatches 4;
206 AA.
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PRT;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE
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Q96M21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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Pred. No. 31,
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                             Query Match 57.7%; Score 41; DB 16; Length 208; Best Local Similarity .58.3%; Pred. No. 12; Matches 7; Conservative 1; Mismatches 4; Indels
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE009587; AALSZ698.1; -
InterPro; IPR000659; Pyridox_oxidase.
Fram; PF01243; Pyridox oxidase; 1.
ProDom; PD006312; Pyridox_oxidase; 1.
ProDom; PD006312; Pyridox_oxidase; 1.
TIGREPMs; TIGR00558; pdxH; 1.
PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
Oxidoreductase; Complete Proteome.
SEQUENCE 208 AA; 23866 MW; CB1F50BC9612DE28 CRC64;
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EMBL, AL627276; CAD06049.1, -
HYpothetical protein; Complete proteome.
SEQUENCE 511 AA; 58126 WW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Glycoprotein gpl20 (Fragment).
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
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Matches 7; Conservative
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Q8Z462
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CSTRAIN=TAINAN 1;

MEDLINE=20074970;

WH U.S.H., Chen B.C.F., Tzen J.T.C.;

Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;

Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;

Tai S.S.K., Pau L.S.H., Tzen J.T., Tzen J.T., Tzen J.T.C.;

S.S.MART, SMO499; AAI; 1.

S.S.GUENCE 148 AA; 1.7524 MW; BA46B033BA13E3DE CRC64;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Boprmatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; eusaterids I; Lamiales; Pedaliaceae; Sesamum.
STRAIN=NJS182;
Brandful J.A.M., Ampofo W.K., Janssens W., Adu-Sarkodie Y.,
Apeagyei F., Anyomi F., Aidoo S., Barnor J.S., Yamamoto N.,
Ishikawa K., Sata T., Kurata T.;
"Genetic and phylogenetic analysis of HIV-1 strains from Southern
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.3%; Score 40; DB 15; Length 81; llarity 66.7%; Pred. No. 7.1; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                             Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AJ225659; CAA12541.1; -InterProf. IPR000777; GP120. Pfam; PF00516; GP120. AIDS, Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 AA; 9138 MW; 2D43DCD554295572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA 1723891 fist clone TESTI2004929.
Homo sapiens (Human).
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es 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 6; Conserv
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Search completed: February 21, 2003, 08:00:44 Job time : 21.6744 secs
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MEDLINE=2054483; PubMed=11016950;

A Sukla H.D. Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Sukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Kaller K., Cruz R., Danson M.J., Hough D.W.,

A landacks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Rendorks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Rendorks T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Blandard H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,

"Genome sequence of Halobacterium species NRC-1.",

"Genome sequence of Halobacterium species NRC-1.",

"Froc. Natl. Acd. Sci. U.S.A. 97:12176-12181(2000).

Rendorks D.G., Rendonel pore.

"InterPro, IPR001646; Speptide repeat.

"InterPro, IPR001646; Speptide repeat.
                                                                                                                       TISSUE=TESTIS;
Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Mishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NIZDO human oDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKOS7453; BAB71493.1;
SEQUENCE 274 AA; 30083 MW; IDD43654D4135BZF CRC64;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.3%; Score 40; DB 4; Length 274; Best Local Similarity 50.0%; Pred. No. 25; Matches 6; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriacae; Halobacterium.
NCBI_TaxID=64091;
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Last annotation update)
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01-WAR-2001 (TrEMBLrel. 16,
01-WAR-2002 (TrEMBLrel. 20,
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Matches 5; Conservative
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66 CFQWRWGVRYLR 77
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SEQUENCE 584 AA
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EMBL, AF028810, AAB88891.1; -.
Hypochetical protein.
SEQUENCE 273 AA, 30986 WW, F195D2FEF7AD44D3 CRC64;
               01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-07-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 31.0 kBa protein.
Rhizobium leguminosarum (biovar viciae).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group;
Rhizobiaceae, Rhizobium.
                                                                                                                                                                                                                                                                        MEDLINE-99113394; PubMed=9914965;
Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.,
Ksenzenko V.N.;
                                                                                                                                                                         STRAIN=VF39;
Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.9%; 'Score 39; DB 2; Length 273; ilarity 60.0%; Pred, No. 37; Conservative 3; Mismatches 1; Indels
01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
6, Conserva
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                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=387;
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25

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Human lactoferrin
Human lactoferrin
Human lactoferrin
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Human lactoferrin
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Human lactoferrin
                                                                                                                                                          February 21, 2003, 07:37:21; Search time 28.093 Seconds (without alignments) 56.918 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Geneseq 101002:*

| S1DS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| S1DS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| S1DS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| S1DS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| S1DS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| S1DS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| S1DS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| S1DS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| S1DS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 CFQWKRNMRKVR 12
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Maximum DB seq length: 200000000
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Human lactoferrin	Human lactoferrin	Peptide for anti-u	lactoferr	lactof	lactof	lactoferr	lactoferr	lactoferr	ctof	lactoferr	lactoferr			1 lactc	ac	n lacto	icrobial p	n-rel	errin	errin d	errin der	rın deri	a lactof	fer	i-parasitic 1	arasitic 1	Peptide for anti-u	oferri	Lactoferrin-derive	errin der	errin-d	oferrin-der	ctoferrin d	arasit	
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21	21	11	21	21	21	21	21	21	21	21	21	12	17	21	21	21	13	14	12	72	15	72	16	16	16	16	17	17	17	17	17		18		
14	14	12	15	15	15	16	16	16	17	17	17	18	18	8 ∺	13	5	20	20	20	20	20	20	50	20	50	20	50	20	20	50	50	70	50	20	
94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	**	<b>T</b>	₹#	٠,	٠.			94.4	_;			94.4		
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11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	6.	44	45	

## ALIGNMENTS

RESULT 1

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Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                      Dolphin GT;
                                                                          Human lactoferrin derived peptide SEQ ID NO:91.
                                                                                                                                                                                                                                                                                                                      Baltzer L,
           AAY78091 standard, Peptide, 12 AA
                                                                                                                                                                                                                                                                                                                      Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                   06-JUL-1998; 98SE-0002441.
17-JUL-1998; 98SE-0002562.
29-DEC-1998; 98SE-0004614.
                                                                                                                                                                                                                                99WO-SE01230.
                                                       (first entry)
                                                                                                                                                                                                                                                                                               (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13.
                                                                                                                                                                                      WO200001730-A1.
                                                                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                06-JUL-1999;
                                                       25-APR-2000
                                                                                                                                                                                                          13-JAN-2000.
                                 AAY78091;
AAY78091
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Human lactoferrin Human lactoferrin Human lactoferrin

AAY78048 AAY78049 AAY78036

AAY78037

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used for treating and can tumours. The peptides can also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 71; DB 21; Length 12; 100.0%; Pred. No. 2.1e-05; ive 0; Mismatches 0; Indels
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                                                            Claim 22; Page 38; 102pp; English.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 100.
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29-DEC-1998;
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Claim 22; Page 38; 102pp; English.

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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uniforms, collife, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                  100.0%; Score 71; DB 21; Length 12; 100.0%; Pred. No. 2.1e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:38.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                               12 AA;
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17-JUL-1998;
29-DEC-1998;
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12 AA;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. It inflammatory acceptational and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used all peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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            Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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fungicidal and bactericidal and may also be used as preservatives
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Pred. No. 9.7e-05;
1; Mismatches 0; Indels
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al Similarity 91.7%;
11; Conservative
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98SE-0004614.
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Best Local Similarity
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                           Human, lactoferrin, modification, infection, inflammation, tumour;
food, infant formula, anti-inflammatory, anti-microbial, anti-tumour;
urinary tract infection, colitis; Candida infection; fungicidal;
bactericidal, preservative.
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          DB 21; Length 12;
Score 67; DB 21; Lens.
Pred. No. 9.7e-05;
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Pred. No. 9.7e-05;
1; Mismatches 0; Indels
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                                      1; Mismatches
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                                                                                                                                                                                AAY78047 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                        11; Conservative
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                                                                      1 CFOWKRINMRKVR 12
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      Query Match
Best Local Similarity
Matches 11; Conserv
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AAY78037 standard; Peptide; 13 AA.

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AAY78001 to AAY78100 represent peptides having sequence based on human latcoferrin. The peptides are taken up in the intestine through the banding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urihary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fundicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                           Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-miorobial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.
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                                                                                                                           Human lactoferrin derived peptide SEQ ID NO:37.
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98SE-0002562.
98SE-0004614.
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                                                                                 (first entry)
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Best Local Similarity 91.7-
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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                                        AAY78037;
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AAY78048
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                                                                                                                                                                                                                                                                                                               Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                           AAY78084 standard; Peptide; 12 AA
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 91.7
Matches 11; Conservative
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1 CFQWERNWRKVR 12
                  1 CFQWQRNMRKVR 12
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17-JUL-1998;
29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                      AAY78084;
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Dolphin GT;

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                                         Gaps
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94.4%; Score 67; DB 21; Length 13; 91.7%; Pred. No. 0.00011; ive 1; Mismatches 0; Indels
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RESULT 7 AAY78037

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         Human, lactoferrin; modification; infection; inflammation; tumour;
food, infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; collitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urrinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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Pred. No. 0.00011;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                       98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB.
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 AA;
                                                                                                                                                WO200001730-A1
                                                                                                Homo sapiens
                                                                                                                                                                                                                       06-JUL-1999;
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                                                                                                                 Synthetic.
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 18; Page 74; 102pp; English.

Dolphin GT;

Baltzer L,

Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB.

98SE-0002441. 98SE-0002562. 98SE-0004614.

06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

99WO-SE01230

36-JUL-1999;

13-JAN-2000

WO200001730-A1

Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment or unimary tract infections. A medicinal product of infections (such as unimary tract infections and/or prevention of infections (such as unimary tract infections, collitis, and candida infections and a membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; collitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.4%; Score 67; DB 21; Length 13; 91.7%; Pred. No. 0.00011; live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                  13 AA;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Company native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.4%; Score 67; DB 21; Length 14; 91.7%; Pred. No. 0.00011; ive 1; Mismatches 0; Indels
                                                                                                          Baltzer L, Dolphin GT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lactoferrin derived peptide SEQ ID NO:50.
                                                                                                                                                                                                                Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78050 standard; Peptide; 14 AA.
                                                                                                         Mattsby-Baltzer I,
              98SE-0002441.
98SE-0002562.
98SE-0004614.
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98SE-0002562.
98SE-0004614.
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                                                                        (ASCI-) A+ SCI INVEST AB.
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                                                                                                                                     WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 AA;
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             06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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17-JUL-1998;
29-DEC-1998;
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                                                                                                         Hanson LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
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Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as universe infections, colitis, and Candida infections (such as universe), inflammations and/or tumours. The peptides can also be used for treating and/or tumours. The peptides can also be used to fulfs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungacidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial; anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal;
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                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 21; Length 14;
Pred. No. 0.00011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:51
   Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                  Claim 15; Page 75; 102pp; English.
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 Mattsby-Baltzer I,
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ilarity 91.7%;
Conservative
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Best Local Similarity
                                 WPI; 2000-147388/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                      14 AA;
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29-DEC-1998;
Hanson LA,
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Gaps . 0

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Claim 18; Page 75; 102pp; English.

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                           AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides an also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The agent is low oln.. It can be
                                                                                                                                                                                        anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                              Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 94.4%; Score 67; DB 17; Length 15; Local Similarity 91.7%; Pred. No. 0.00012; les 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - has low toxicity, is
                                                                                                                                                                                                                                                                                                                          Score 67; DB 21;
Pred. No. 0.00011;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-ulcer agent contg. peptide -
heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 11; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                            94.4%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide for anti-ulcer agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94JP-0283869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             3 CFQWQRNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                             Sequence
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment or through the circulation. A medicinal product of the peptide or fragment or membrane), inflammerions and/or prevention of infections (such as uninary tract infections, colitis, and Candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

The though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; untinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.4%; Score 67; DB 21; Length 15; 91.7%; Pred. No. 0.00012; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolphin GT,
                                                                                                   Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baltzer L,
AAY78035 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78062 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                 98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                 99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASCI-) A+ SCI INVEST AB.
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Best Local Similarity
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                                                                                                                                                                                                                                                                            WO200001730-A1.
                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998;
29-DEC-1998;
                                                                  25-APR-2000
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                                 AAY78035;
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Matches
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AAY78062
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Gaps

Best Loca Matches

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the carcific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infections (such as mebrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also through and actericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used all inically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would costs. Therefore, provision of peptides based on lactoferrin at lower
                                                                                Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
uvrinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                 Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 81; 102pp; English
                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                     99WO-SE01230
                 25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 AA;
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                                                                                                                                                                                                                                                                                                                                    06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                             Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                 13-JAN-2000
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Dolphin GT;

0; Gaps Query Match

94.4%; Score 67; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.00012;
Matches 11; Conservative 1; Mismatches 0; Indels

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1 CFOWKRNMRKVR 12 CFOWORNMRKVR 15 Search completed: February 21, 2003, 07:56:44 Job time: 28.093 secs

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Sequence 3, Application US/08204487

Patent No. 556425

GENERAL INFORMATION:
APPLICANT: NAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MARKINA, HIDEKI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: TAMAKA, SHIGBAKI
APPLICANT: TAWASAKI, YOSHINIRO
APPLICANT: NAWASAKI, YOSHINIRO
APPLICANT: NAWASAKI, YOSHINIRO
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATERT ADMINISTRATOP
STREET:
ATREET: THISPAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: UZ109
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: US-MAR-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL: PAULA A.
REGISTRATION NUMBER: 32,503
REGISTRATION NUMBER: 32,503
REGISTRATION NUMBER: 32,503
RELERRAN: (617) 248-7100
TELERRAN: (617) 248-7100
TELEBRAN: (617) 248-7100
TELEBRAN: (617) 248-7100
THORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
             US-08-406-271-2
US-09-421-6386-2
US-09-421-6386-2
US-09-932-190-2
US-08-655-640-4
US-08-655-640-4
US-08-461-333-4
US-08-461-333-4
US-08-461-333-4
US-08-461-333-4
US-08-456-108-2
US-08-256-308-2
US-08-256-108-2
US-08-456-108-2
US-08-456-108-2
US-08-456-108-2
US-08-456-108-2
US-08-456-108-2
US-08-456-108-2
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single
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LOCATION: 1..18
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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RY: USA
02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
 699
                                                                                        February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39:537 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Sequence 1, Sequence 24,
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Seguence 3,
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Sequence 1
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  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
  /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
  /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
  /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
  /cgn2_6/ptodata/1/iaa/PoTUS_COMB.pep:*
  /cgn2_6/ptodata/1/iaa/PoTUS_COMB.pep:*
           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-68-98-8
US-08-68-98-8
US-08-68-98-8
US-07-95-161A-3
US-07-91-174-3
US-07-91-174-3
US-08-204-487-1
US-08-26-771-25
US-08-26-771-25
US-08-381-984-25
US-08-381-984-25
US-08-381-984-25
US-09-508-734-6
US-07-91-174-4
US-07-91-174-10
US-07-91-174-8
US-07-91-174-8
US-07-91-174-8
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US-07-91-174-8
US-07-91-174-8
US-08-26-771-30
US-08-271-6
US-08-69-271-6
US-08-66-271-6
US-08-66-271-6
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                                                                                                                                                                                                                                              262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                         1 CFOWKRNMRKVR 12
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length: 20000000000
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Match Length
                                                                                                                                              Title:
Perfect score:
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Maximum DB seq
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PATEUR NO. 2931341

APPLICANT: VLASONG MING
APPLICANT: CERAMI, ANTHONY
TITLE OF INVESTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESCONDENCE ADDRESS:
ADDRESSES: Klauber & Jackson
GITY: Hackensack Avenue
CITY: Hackensack Avenue
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: April 4, 1996
CLASSIFICATION: 514
ATTORNEY/ARION NUMBER: US 08/418,642
FILING DATE: APPLICATION: 514
ATTORNEY/AROMINICATION INDERRY: 20.442
REGISTRATION NUMBER: 26.742
REGISTRATION NUMBER: 26.742
REGISTRATION NUMBER: 26.742
REGISTRATION NUMBER: 27.5800
TELEFROME TREERY: 201.443-1684
TELEX: 133521
TELEX: 133521
TELEX: 133521
TELEX: 133521
TELEX: Mainto acid
TELEX: Anion acid
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Sequence 8, Application US/08475055

Sequence 8, Application US/08475055

GENERAL INFORMATION:

APPLICANT: YONG MING LI

APPLICANT: HILEN VLASSARA

APPLICANT: ANTHONY CERAMI

TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: AND PRODUCTS, AND METHODS OF THEIR USE

NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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91.7%; Pred. No. 9.9e-05;
                                                                                                                                            Sequence 8, Application US/08628380
Patent No. 5891341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECTIE TYPE: Peptide DESCRIPTION: LF-C1, 8-25 HYPOTHETICAL: NO
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Best Local Similarity 91.7
Matches 11, Conservative
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; FRAGMENT TYPE: internal
US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: YOUR MING LI
APPLICANT: HELEN VLASSRAA
APPLICANT: HELEN VLASSRAA
APPLICANT: HELEN VLASSRAA
APPLICANT: HELEN VLASSRAA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack
STREET: 411 Hackensack
STRIE: New Jersey
                                                                                                                   Query Match 94.4%; Score 67; DB 1; Length 18; Best Local Similarity 91.7%; Pred. No. 9.9e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 0'601

COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
94.4%; Score 67; DB 2;
Best Local Similarity 91.7%; Pred. No. 9.9e-05
Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPPLICATION: 436
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7,1995
FILING DATE: APRL 7,1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION: 436
ATTORNEY/AGENT INFORMATION: AREFERENCE/DOCKET NUMBER: 947-1-TELECOMMUNICATION INFORMATION: TELEFONK: 201 487-5800
TELEFONK: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TTREE amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                internal
                                                                                                                                                                                                                                                     1 CFOWKRINMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFOWKRNMRKVR 12
                                                                                                                                                                                                                                                                                               1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-485-948-8
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Gaps

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MAP POSITION:

UNITS:

WARTED

WATE

UNITS:
FRATURE:

NAME/KEY:
MANE/KEY:
MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67;
                                                                                                     US/07/755,161A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
                                                                                                                            FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: WALTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
TELEFAX: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.48;
                OPERATING SYSTEM: MS-DOS
                                          SOFTWARE: DisplayWrite CURRENT APPLICATION DATA: APPLICATION NUMBER: US/FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN:
INDIVIDUAL ISOLATE:
DBVELOPHENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL INPE:
CRLL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1:
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPENDENCE ADDRESS:
ADDRESSE; Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
STREET: B.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MADIUM TYPE: Diskette, 5.25 inch, 500Kb
                                                                                                                                                COUDTER: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 94.4%; Score 67; DB Best Local Similarity 91.7%; Pred. No. 9.9e Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/485,948
FILING DATE:
FILING DATE: 07087,1395
APPLICATION NUMBER: 08/418,642
FILING DATE: 07087,1395
APPLICATION NUMBER: 08/418,642
FILING DATE: 07087,17,1995
CLASSIFICATION: 07088TI 7,1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 96,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18708ARTION:
TELECOMMUNICATION 18708ARTION:
TELEFAX: 201 343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FRAGMENT TYPE: internal US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-07-755-161A-3
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LOCATION: 2

LIDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 19"
FRATURE: NFORMATION: thiol group of Cys residue at location 19"
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond witl OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NOSUCHI, WATRAU
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIMIRO
APPLICANT: KAWASAKI, YOSHIMIRO
APPLICANT: KAWASAKI, YOSHIMIRO
TITLE OF INVENTION: UNRAL INPECTION AND PROLIFERATION
TITLE OF INVENTION: UNHIBITORS
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: ABABLE FORM:
MEDIUM TYPE: ILOPPY disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTION NUMBER: 02-MAR-1994
CLASSIFICATION NUMBER: 32,503
REFIRERUCE/DOCKET NUMBER: FUN-019
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67; DB 1; Length 20;
Pred. No. 0.00011;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE:
DOCUMENT NUMBER:
FILING DATE:
FULING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08204487
Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWKRINMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                       TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
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                                 Gaps
                                 ö
       Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                           Sequence 3, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Peptides and an IITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STRRET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: WESTINGON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compactible
COMPUTER: IBM Compactible
COMPUTER: DISPLAYWHITE
OFFRATING SYSTEM: MS-DOS
SOFFWARE: DISPLAYWHITE
CHRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION NUMBER: US/07/85,161
ATTORNEY/AGBRT IRFORMATION:
APPLICATION NUMBER: US
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
RELEPHONE: 202-371-8856
TELLEPAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FUNITS:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                        1 CFOWKRNMRKVR 12
                                                                                                            2 CFOWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                       RESULT 6
US-07-891-174-3
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Gaps
                                                                                                                                                                                                                                                           Sequence 25, Application US/08256771
Patent No. 5565591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENITON: ANTIMICROBIAL AGENTS AND METHOD FOR IREATING
TITLE OF INVENITON: PRODUCTS THEREMITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderchi, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                           Score 67; DB 1; 1
Pred. No. 0.00011;
1; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 67; DB 1; I
Pred. No. 0.00011;
1; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: Moraperitect 5.1
COMPUTER: Moraperitect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATYORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                           94.4%;
illarity 91.7%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear WOLECULE TYPE: peptide
                                                                                                                       1 CFQWKRNMRKVR 12
                                                                                                                                                                 2 CPOWORNWRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
                                           Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si:
      US-08-256-771-24
                                                                                                                                                                                                                         RESULT 9
US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-381-984-24
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Patent No. 565691

GENERAL INFORMATION:
APPLICANT: Mannoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING ITILE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES. 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
GITY: Mashington
                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                   Score 67; DB 1; Length 20;
Pred. No. 0.00011;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                       /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: TESTINGOUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: UJY 22, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
RICHARD APPLICATION DATA:
APPLICATION NUMBER:
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24:
                                                                                                                                                                                                                                                                                                   94.4%;
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INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
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MOLECULE TYPE: peptide
                                                                                                                                                                             NAME/KEY: Peptide
COATION: 1..20
OTHER INFORMATION:
COTHER INFORMATION:
US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                         2 CFQWQRNMRKVR 13
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Sequence 4, Application US/09508734

Sequence 4, Application US/09508734

Sequence 4, Application US/09508734

Sequence 4, Application US/09508734

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION:
USeful microorganism thereof
FILE REFERENCE: PA/SYG/00137

FRICK APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment ther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
| LOCATION:
| IDBNITECATION NETHOD:
| OTHER INFORMATION: /note= "cysteine residues at positions 2
| OTHER INFORMATION: /note= "cysteine residues at positions 2
| OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.00011;
1; Mismatches 0; Indels
                                                                                                                                   ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
FILING DATE: April 11, 1995
TILING DATE: THORNATION:
NAME: WAITEN M. Cheek, Jr.
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELEFAK:
TELEFAK:
TELEFAK:
TELEFAK:
              805 Fifteenth Street, N.W., #700
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INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 20 antho acids
TYPE: antho acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7
Matches 11, Conservative
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                                              Washington
                                                                                                              U.S.A.
                                              CITY: Was
STATE: D
COUNTRY:
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US-09-508-734-4
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thered
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
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Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE MEDERSS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                        ZUP: 2005
ZUP: 2005
ZUP: 2005
ZUP: 2006
ZUP: 2
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Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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NAME/KEY:
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US-08-381-984-25
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NAME/KEY: modified site
LOCATION: 21
LOCATION: 21
LOCATION: 21
LOCATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cyg residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cyg residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10
     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren W. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE:
POSITION IN GENOME:
CHROMOSCOME/SEGMENT:
MAP POSITION:
UNITS:
FRATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
                                                                                                                                                                                                              TELEX:
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERRETICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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VOLUME:
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                                                                                                                                      Score 67; DB 4; Length 22;
Pred. No. 0.00012;
1; Mismatches 0; Indels
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US-07-755-161A-10

Sequence 10, Application US/07755161A

Sequence 10, Application US/07755161A

PAPEL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES:

NUMBER OF SEQUENCES:

ADDRESSPONDENCE ADDRESS:

ADDRESSPONDENCE ADDRESS AD
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIORA APPLICATION DATA;
APPLICATION NUMBER:
                                                                                                                                 Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4
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Matches 11; Conserva
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Gaps .. 0

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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond wit)
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 94.4%; Score 67; DB 1; Length 25; Best Local Similarity 91.7%; Pred. No. 0.00013; Matches 11; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
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                                                                                                                                                                                                                               TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
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LOCATION: 4
LOCATION: 4
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: Cys residue of Cys residue at location 21"
        RESULT 15
108-07-891-174-10
108-07-891-174-10
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ADDRESSES: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STRATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IEM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: DISPLAYMITE COMPUTER: IEM COMPUTER: DISPLAYMITE COMPUTER: PROCOMMER: US/07/891,174 FILING DATE: 29-MAX-1992
CLASSIFICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Check Jr.
REGISTRATION NUMBER: 33,367
REJERHANE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGHT: 25 amino acids TYPE: AMINOLOGY: linear MOLECULE TYPE: HYPOTHETICAL: ANTI-SENSE: FRAGMENT TYPE: ORIGINAL SOUNCE: ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: modified site.
LOCATION: 21
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL INVE:
ORGANELLE:
INMEDIATE SOURCE:
LIBRARY:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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TYPE: PRT
CORGANISM: HOMO SAPIENS
US-09-798-869-2
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                        RESULT 2
US-09-798-869-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                          February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

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13: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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US-09-738-626-5715
O US-09-925-301-1246
US-09-978-295A-119
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US-00-023-066-2
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US-09-798-869-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                     156504 seqs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                     Copyright
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Match 1
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Perfect score:
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No.
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20 37 52.1 338 9 US-09-978-697-119 Sequence 119, App 22 37 52.1 338 9 US-09-998-1821-119 Sequence 119, App 22 37 52.1 338 9 US-09-998-1832A-119 Sequence 119, App 22 37 52.1 338 9 US-09-998-1832A-119 Sequence 119, App 22 37 52.1 553 10 US-09-981-649A-24 Sequence 119, App 22 37 52.1 553 10 US-09-981-649A-30 Sequence 24, App1 22 37 52.1 554 10 US-09-981-649A-30 Sequence 24, App1 29 37 52.1 554 10 US-09-981-649A-30 Sequence 24, App1 30 US-09-981-649A-28 Sequence 27, App1 31 32 35 49.3 30.1 0 US-09-881-649A-28 Sequence 28, App1 31 32 32 35 49.3 30.1 0 US-09-881-649A-28 Sequence 39, App1 32 35 49.3 30.1 0 US-09-881-649A-28 Sequence 38, App1 34 49.3 10.13 9 US-10-121-049-38 Sequence 38, App1 36 49.3 10.13 9 US-10-121-049-38 Sequence 38, App1 37 35 49.3 10.13 9 US-10-175-746-38 Sequence 38, App1 39 35 49.3 10.13 9 US-10-176-918-38 Sequence 38, App1 40.3 10.13 9 US-10-176-918-38 Sequence 38, App1 39 35 49.3 10.13 9 US-10-176-918-38 Sequence 38, App1 40.3 10.13 9 US-10-176-918-38 Sequence 38, App1 41.3 47.9 62 10 US-09-815-242-13026 Sequence 130.26, App1 42 34 47.9 62 10 US-09-815-242-13026 Sequence 130.26, App1 42 34 47.9 69 US-09-815-242-13026 Sequence 130.26, App1 44 47.9 69 US-09-815-242-13026 Sequence 130.26, App1 44 47.9 69 US-09-815-242-13026 Sequence 130.26, App1 45 34 47.9 69 US-08-915-242-
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## ALIGNMENTS

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Sequence 2. Application US/09798869
; Sequence 2. Application US/09798869
; Publication Wo. US2033022821A1
; GBMERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDEN
APPLICANT: BALDUN SVENDAL
APPLICANT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-28
PRIOR PILING DATE: 1999-08-28
; NUMBER OF SEQ ID NOS: 30
SOFTWARE: PRI
APPLICANT: LS
TYPE: PRI
APPLICATION US/09798869
; SEQUENCE 20, Application US/09798869
; PUBLICANT: GYSTEN REKDAL
APPLICANT: GARREAL INPORMATION:
APPLICANT: GYSTEN REKDAL
APPLICANT: BALDUN SUENDEN
APPLICANT: BALDUN SUENDEN
APPLICANT: BALDUN SUENDEN
APPLICANT: BALDUN SUENDEN
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; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens ; OTHER INFORMATION: sequence)
US-09-798-869-6
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Query March 94.4%; Score 67; DB 9; Length 694; Best Local Similarity 91.7%; Pred. No. 0.0017; Matches 11; Conservative 1; Mismatches 0; Indels
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Pred. No. 0.001;
1; Mismatches 1; Indels
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Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OOHN SIGURD SVENDEN
APPLICANT: BALDUR SVENDAL
APPLICANT: BALDUR SVENDAL
APPLICANT: LARS VORLAND
ITTLE OF INVENTION: BLOACTIVE PEPTIDES
ITTLE OF INVENTION: BLOACTIVE PEPTIDES
CURRENT PILING DATE: 2001-02-7
FRIOR PELICATION NUMBER: CT/GB99/02851
PRIOR FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: GP8818938.4
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR APPLICATION NUMBER: G99-08
NUMBER OF SEQ ID NOS: 30
SOFTWARR: FARENCE 1598-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARR: FARENCE 1598-08-28
ILENGTH: 15
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JUS-09-7, 58-50-7-9
JUS-09-7, 58-50-7-9
JUS-09-7, 58-50-7-9
JUDICATION NO. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OGHN SIGUED SVENDSEN
APPLICANT: EALDUE SVENDAL (RNSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02651
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1990-08-36
JUMBER OF SEQ ID NOS: 30
SOFTWARE: FABELSEQ for Windows Vergion 4.0
SSOFTWARE: PABELSEQ for Windows Vergion 4.0
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83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                    22 CFOWORNMRKVR 33
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                                                                                                    1 CFOWKRINMRKVR 12
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Best Local Similarity
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US-09-798-869-3
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APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67; DB 9; I
Pred. No. 8.2e-05;
1; Mismatches 0;
     APPLICANT: LARS VORLAND
TITLE OF INVENTION: BLOACTIVE PEPTIDES
TITLE REPERENCE: A34049-PCT-USA-A;
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PASLEREQ for Windows Version 4.0
SEQ ID NO. 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10505/P58185C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAX-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REPROSMYUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10023096
Patent No. US20020160941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           ch 94.4%; Similarity 91.7%; 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 694 amino acids
amino acid
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US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWKRINMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CFOWORNMRKVR 14
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Matches
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Gaps

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Score 41; DB 9; Length 25; Pred. No. 1.3; 3; Indels 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                  APPLICANT: (YSTEIN REKDAL APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: (YSTEIN REKDAL APPLICANT: (YSTEIN REKDAL APPLICANT: BALDOR SVEENBJ (RNSSON APPLICANT: LARS VORLAND: TITLE OF INVENTION: BIOACTIVE PEPTIDES FILE REFERENCE: A34049-PCT-USA-ACURRENT APPLICATION NUMBER: US/09/798,869 CURRENT FILING DATE: 1999-08-31 PRIOR APPLICATION NUMBER: CTJG99/02851 PRIOR APPLICATION NUMBER: GB9918938.4 PRIOR FILING DATE: 1999-08-28 NUMBER OF SEQ ID NOS: 30 SEQ ID NOS: 30 SEQ ID NOS: 30 LENGTHRE: PSELEGE FOR Windows Version 4.0 SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVETNED (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A4049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 22
LIENGTH: 25
                                                                                                                                                        Sequence 4, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
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Best Local Similarity 54.5
Matches 6; Conservative
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  1 CFOWKRNMRKV 11
                                              3 CYÓWOWRMRKL 13
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Best Local Similarity
Matches 6; Conserv
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; ORGANISM: MURINE
US-09-798-869-22
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; ORGANISM: MURINE
US-09-798-869-4
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OTHER INFORMATION: synthetic peptide (modified form of homo sapiens;
OTHER INFORMATION: sequence)
US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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  1; Indels
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APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BLOACTIVE PEPTIDES
TITLE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/796,869
CURRENT PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938-4
PRIOR PILING DATE: 1998-08-31
PRIOR PLING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FABELSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 15
  3; Mismatches
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FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION WHERE: US/09/798,869
CURRENT FILING DATE: 2001-02-2/7
PRIOR APPLICATION WHORER: PCT/GB99/02851
PRIOR PLING DATE: 1999-06-31
PRIOR PLING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                           US-09-798-869-23
Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SYENDSEN
APPLICANT: GYSTEIN REKDAL
APPLICANT: BALDUK SVEINED (RNSSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09798869 Publication No. US20030022821A1
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ORGANISM: Artificial Sequence
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Matches 7; Conservative
7; Conservative
                                                                        3 CYQWQRRMRKL 13
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                                              1 CFQWKRNMRKV 11
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ORGANISM: CAPRINE
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LENGTH: 25
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  Matches
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CTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine creek INFORMATION: sequence)
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US-09-798-869-29

Sequence 29, Application US/09798869

Sequence 29, Application US/09798869

Sequence 29, Application US/09798869

Sequence 29, Application US/0979869

Publication No. US20030022821A1

APPLICANT: GYETEIN REKDAL

APPLICANT: BALDUK SVEINBJ(RNSON APPLICANT: BALDUK SVEINBJ(RNSON APPLICANT: BALDUK SVEINBJ(RNSON APPLICANT: BALDUK SVEINBJ(RNSON APPLICANTON)

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FABLESE FOR WINDOWS VERSION 4.0

SSOFTWARE: FABLESE FOR WINDOWS VERSION 4.0
                                                                                                                                                                     MENOUT 109-798-869-8

Sequence 8, Application US/09798869

Publication No. USZ0030022821A1

SEDERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: AREX VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US/0999/02851
PRIOR APPLICATION NUMBER: US/0999/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PLING DATE: 1998-08-31
PRIOR PLING DATE: 1998-08-38

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FASLEED FOR Windows Version 4.0

SEQ ID NO 8

SEQ ID NO 8

SEQ ID NO 8

SEQ ID NOS: 30
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWKRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CLRWOWEMRKV 13
1 CFOWKRNMRKV 11
                                                 48 CYGWKRNNKGV 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

54.9%; Score 39; DB 9; Length 333;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                          GENERAL INVEGRATION SCHOOL SECRETED PROTEINS AND USES THEREOF TITLE OF INVERTATION SECRETED PROTEINS AND USES THEREOF TITLE OF INVERTION SECRETED PROTEINS AND USES THEREOF TITLE OF INVERTION SECRETED PROTEINS AND USES THEREOF TITLE OF INVERTION SECRETED S
                                 s-09-796-753-26
Sequence 26, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
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; ORGANISM: Mouse
US-09-796-753-26
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53.5%; Score 38; DB 9; Length 15; 45.5%; Pred. No. 2.4; tive 4; Mismatches 2; Indels
       93.5
Best Local Similarity 45.5
Matches 5; Conservative
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APPLICANT: Desarber, Andrea E.
APPLICANT: Maluli, Khisimuai
APPLICANT: Maluli, Khisimuai
APPLICANT: Bekker, Linda-Gail
APPLICANT: Beker, Linda-Gail
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secritetary of the
APPLICANT: as represented by The Secritetary of the
APPLICANT: Department of Health and Human Services
TITLE REFERENCE: 015280-413100US
CURRENT PEPLICATION NUMBER: US/09/889,320
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
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/ ORGANISM: Mycobacterium tuberculosis
/ OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

OTHER INFORMATION: MART TO ALG96701.14

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN H474, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, BIGNAL = 1.6

US-09-864-761-47985
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Pred. No. 3.3;
1; Mismatches 0; Indels
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Pred. No. 59;
2; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PRILING DATE: 2000-09-21
PRIOR PRILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 47985
LIGHTH 21
LIGHTH 21
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Publication No. US20030013090A1
GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 5; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
5, Conserve
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Sequence 47985, Application US/09864761

Patent No. US20020048763A1

### APPLICANT: Perm's David R.

### APPLICANT: Benn, Sharron G.

### APPLICANT: Chen Wensheng

#### APPLICANT: Chen Wens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Length 15;
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Pred. No. 2.4;
4; Mismatches
                                                                                                                                                                                                                                                                     APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: VETEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
TITLE OF INVENTION: BLOACTIVE PEPTIDES
FILE REFERENCE: A3404-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB8818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSSLEEQ for Windows Version 4.0
SED ID NO SSCIEN WINDOWS VERSION 4.0
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                                                                                                                                                                               Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWKRNMRKV 11
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                 3 CFRWOWRMKKL 13
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; ORGANISM: BOVINE
US-09-798-869-30
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Search completed: February 21, 2003, 08:11:56 Job time : 6.88372 secs

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n Ltd.		n time 10.6047 Seconds alignments) Million cell updates/sec				283224				y chance to have a e result being printed, distribution.		Description	ing in	hypothetical prote	pyridoxamine 5'-ph pyridoxamine 5'-ph	probable pyridoxam hypothetical prote	9 5	dynein beta heavy	hypothetical prote	ribosomal protein	ribosomal protein	hypothetical prote	probable monooxyge	268 proteasome SU	apolipoprotein B-1	hypothetical prote T14P4.7 protein -	probable cytochrom hypothetical prote
Core version 5.1.3 1993 - 2003 Compugen	ng sw model	3, 07:48:01 ; Searc (without 108.784	2, 2,	Gapext 0.5	34422 residues	chosen parameters:	00	18 .00% .5 summaries		results predicted by il to the score of the of the total score d	SUMMARIES	ID	TFHUL JC2323	T22597	AB2670	AG3441 AB0858	A28438	T08030	G86506	6/2115 A48396 att 201	AH1673	S//802 AD2346	C70655	E C C C C C C C C C C C C C C C C C C C	80.7989 B60950	T22879 B86156	B84514 T24218
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	n - pr		score:	able:		number of	DB sed DB sed	essing		26.8		Score	φ ις, «	* 4	4 <b>4</b>	4, 4, L L	4.4	04.0	n m c	n co c	0 00 0	20 00 00 71 PM P	0 00 0	2.6.0	) W (	37	37
	OM protei	Run on:	Title: Perfect s Sequence:	Scoring t	Searched:	Total num	Minimum D Maximum D	Post-proc	Database	Pred score and	i	Result No.	чач	ባቴ፣	nφ	r- 89	ο -	11:	13.	# 45 F	17	9 6 C	22.0	23.6	4 (2) (	27	2 28 2 9 8

hypothetical prote GTP-binding regula hypothetical prote trichhyalln like hypothetical prote hypothetical prote F151.22 (imported hypothetical prote 60S ribosomal prot hypothetical prote pre-pilin ledder p 33.3K hypothetical prote hypothetical protect hypothetical hypot	SINE	RESULT 1 TFHUL lactotransferrin precursor [validated] - human N,Alternate names: lactoferrin C;Species: Romo sapiens (man) C;Dacies: Romo sapiens (man) C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000 C;Accession: G01394; S11228; Ā45401; S10324; S15853; S20841; S07160; A61169; A31000; S	. 7661	айвг/оовд	86; PIDN:AAB60324.1; PID:g467237 Pieper, F.R.	uman mammary gland lactoferrin. PMID:2402455	REY> 5; PIDN:CAA37914.1; PID:G34416 : Panella. T.	of the estrogen action that regulates lactofe PMID:1480183	PIDN: AAB24877.1; PID:9263312		oferrin cDNA. DMTD-2374734		, PIDN:CAA37116.1; PID:934412 veedie, J.W.	errin in baby-hamster kidney cells. PMID:2049066	not compared with conceptual translation	
T17324 S52418 T28820 T28820 B85431 AG1343 AG1343 AG1343 T09680 G98020 G98020 G986403 T126882 T126882 T126871 I37477	ALIGNMENTS	dated] - hu vision 21-h	ry, March	d from GB/F	NID:946723 Der, H.A.;	lence of h	,424-711 NID:934419 Walmer. D.	992 nechanism :93125571;	ID:9263311	NCBI backbo	o numan lacto		NID:934411 k, W.D.; Tv	nan lactofe :91264786;	not shown;	Δ.
принатирически		alic n re- A454	bra.	ate	43; deBo	segu	61; 61;	ar t	ż.	ta om 1	199( of 1		41; Funl	hur GID	G L	ST2;
8858 9980 1129 9990 1129 1289 1319 1419 1419 1419 1419		rsor [v. toferri s (man) equence	Data Li 6820	transl	BL:U076	eotide 1228; M	150-422 BL:X539 Yang.	69-1981 molecul 5401; M	.852659	placen	J.E. 4013, quence		BL:X529 T.A.;	55, 199 cloned 5853; M	seguen	in 30-31 <
00000000000000000000000000000000000000		n precu: ss: lac sapien 1992 #s	e EMBL Der: GO	minary; mRNA	ces: EM loshuk,	te nucl	mRNA mRNA 18, T', ces: EM	6, 19 ential per: A4	5 4 01 DNA C < TEN>	source:	Ogden, es. 18, tide ser	0324 : mRNA	11 < POW ces: EM ; Rado,	sion of ser: Sl	5853 ic acid : mRNA	31 <st1 0841 : prote 28,'X',</st1 
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		nsferrinate names: Homo	to the	prelin	W. Wo	Comple	lon: SI le type 98: 1-1. referen	ocrinol Differ	lon: A4 le type ss: 1-1	nental	Acids Re Nucleo	ion: S1	es: 3-7 referen L, K.M.	J. 276 Expres	nucle:	es: 20-1 lon: S2 le type le type
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		RESULT 1 TEHUL Lactotran N,Alterna C,Species C,Date: 3 C,Accessi	ubmitted Referency Accessi	Status:	Cross-1; Rey, M.	Title:	, Access , Molecul , Residue , Cross-1	ol. Endc	Accessi Molecul Residue	, Experin	.,Powell, ucleic ? .,Title:	, Accessi , Molecul	Residue Cross-1 Stowell	iochem. ;Title: ;Referer	, Accessi , Status: , Molecul	Residue Accessi Molecul Residue

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lactoferrin - sheep (fragment)
[Species ovis orientalis aries, Ovis ammon aries (domestic sheep)
[C,Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
[C,Date: 14-Jul-1995]
[B,Date: 14-Jul-1995]
[B,Date: 14-Jul-1995]
[B,Date: 14-Jul-1995]
[B,Date: 14-Jul-1995]
[B,Date: 15-Jul-1995]
[B,Date: Biophys. Acta 1243, 25-32 1995]
[B,Date: Biochim. Biophys. Acta 1243, 25-32 1995]
[B,Date: Book of a sheep lactoferrin, an inhibitor of platelet A,Reference number: S52107; MUID:95127729; PMID:7827104
[B,Date: Brellminary
[B,Molecule type: protein]
[B,Molecule type: Drotein]
[B,Date: Brellminary
[B,Date: Brellminary]
[B,Date: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL;Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A;Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .Species: Caenorhabditis elegans
|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
|Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Nap position: X
A;Introns: 67/1;153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                              Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 33;
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                                                                                                              Indels
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A.Refession: T22597
A.Status: preliminary; translated from GB/EMBL/DDBJ A.Residues: 1-275 AMILS.
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                                   70.4%; Score 50; DB 2; 63.6%; Pred. No. 0.72;
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Pred. No. 0.12;
                                                                                                                   3; Mismatches
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54.5%;
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                                                                                                                                                                                                       1 CFQWKRNMRKV 11
                                                                                                                                                                                                                                                                                      38 CYQWORRMRKL 48
                                   Query Match
Best Local Similarity
Matches 7; Conserv
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A;Recession: S07160
A;Recession: S07160
A;Rocession: S07160
A;Rocession: S07160
A;Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
B;Panella, T.G.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-343, 1991
A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyth A;Reference number: A61169; MUID:91235214; PMID:1674448
A;Reference number: A61169; MUID:91235214; PMID:1674448
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C,Superfamily: transferrin; transferrin repeat homology
C,Superfamily: transferrin; transferrin; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-71/Product: lactoriansferrin sequence #status experimental <MAT>
F;20-11/Product: lactoriansferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;29-65,39-56,135-218,171-199,190-201,551-265,530-697,595-609/Disulfide bonds: #status F;157,498,Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
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A,Residues: 3-701, SWKPVN' <PAN>
Experiental source: normal breast tissue
R,Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Eur. J. Biochem. 145, 659-666, 1984
A,Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A,Reference number: A31000, MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A;Note: this is the final paper in a series
A;Note: this is the final paper in a series
B;Houen, G:; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Eur. J. Biochem. 241, 33-308, 1996
A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
A;Reference number: S74119; MUID:97054624; PMID:8898921
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A,Rolecule type: mRNA
A,Residues: 1-708 «LRP>
C,Superfamily: transferrin; transferrin repeat homology
C,Keywords: duplication; glycoprotein
F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 20-Reb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
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ilarity 91.7%; Pred. No. 0.00075;
Conservative 1; Mismatches 0; Indels
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: GDB:119368; OMIM:150210
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nes 11; Conserv
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Length 208;

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Score 41; DB 2;
Pred. No. 8.3;
1; Mismatches
     A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME11517
A;Map position:
A;Superfamily: pyridoxamine-phosphate oxidase
C;Keywords: oxidoreductase
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58.3%;
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
7; Conserve
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A,Molecule type: DNA
A,Residues: 1-511 <PAR>
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain CSB, C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Acession: AB2677; PMID:11743193
A;Acession: AB2670
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 < KUR>
A;Residues: 1-206 < KUR>
A;Cross references: GB:AE008688; PIDN:AAL41776.1; PID:g17739129; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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A;Residues: 1-208 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52698.1; PID:g17983525; GSPDB:GN00190
                                                                                                                                                                                                    A;Residues: 1-206 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
C;Accession: AG3441
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Pred. No. 8.2;
1; Mismatches
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A;Map position: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase
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C; Superfamily: pyridoxamine-phosphate oxidase
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58.3%;
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Best Local Similarity
Matches 7; Conserva
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                                                                                                                              A;Accession: H97451
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C; Species: Salmonella enterica subsp. enterica subsp. enterica subsp. enterica serovar C; Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: ABG858
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche H; T., T., Connetron, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra, S.; Monle, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servant A;Reference number: ABS502; PMID:11677608
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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A4128.
B;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactorransferrin is the major estrogen inducible protein of mouse uterine secon A;Reference number: A92596; MUID:87280033; PMID:3611056
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A,Residues: 3-707 <PRN-
A,Cross-references: EMBL:003298
R,Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A,Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A,Reference number: A41205, MUID:92042099; PMID:1939212
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C;Superfamily: transferrin; transferrin repeat homology
C;Reywords: duplication; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
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Pred. No. 20;
0; Mismatches
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CyAccession: G86506
Rishirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311–2314, 2000
A,Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A,Racession: G86506
A,Racession: G86506
A,Racession: G86506
A,Racession: A,Racession: A,Racession: G86506
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
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A;Experimental source: strain J138
                                                                                                                                                                                                                                                                                                        hypothetical protein M18.8 - Caenorhabditis elegans
hypothetical protein M18.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T18633; T23799
A;Accession: T18633
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T18633
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-447 <WILL>
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A;Experimental source: clone B0001
B;Steward, C.
B;Steward, C.
A;Reference number: 219800
A;Reference number: 219809
A;Steus: preliminary; translated from GB/EMBL/DDBJ
A;Steus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.447, ~4M2>
A;Cross-treferences: EMBL:Z68507; PIDN:CAA92831.1; GSPDB:GN00022; CESP:M18.8
A;Experimental source: clone M18
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A;Introns: 41/3; 137/1; 326/3; 434/2
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1852 CFQWQSQLRYIQ 1863
                                      1 CFOWKRINMRKVR 12
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291 WKRNLREV 298
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A;Gene: CESP:M18.8
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A,Gene: CPj0126
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Cypecies: Otherwydomonas reinhardtii
Cypecies: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
CyAccession: T08030
CyAccession: T08030
CyAccession: T08030
CyAccession: T08030
Ayritle: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
Ayritle: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
Ayreference number: Z16302; MUID:94274778; PMID:8006077
Ayreference number: Alford GB/EMBL/DDBJ
Ayrolecule type: DNA
Ayreferences: EMBL:U02963; NID:940965; PIDN:AAA19956.1; PID:9514215
Ayross-references: EMBL:U02963; NID:940965; PIDN:AAA19956.1; PID:9514215
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A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 334/3; 334/3; 368/3; 388/3; 21004/3; 1115/3; 234/3; 324/3; 368/3; 388/3; 21004/3; 1115/3; 21004/3; 1115/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3; 21004/3
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F;20-707/Product: lactotransferrin #status predicted <MAT>
F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                          57.7%; Score 41; DB 1; Length 707; llarity 54.5%; Pred. No. 28; Conservative 2; Mismatches 3; Indels
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4; Mismatches 3; Indels
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A,Gene: ODA4
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RiKalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

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Nature Ganet. 21, 385-389, 1999

A; Rieference number: A72000; MUID:99206666; PMID:10192388

A; Reference number: A72000; MUID:99206666; PMID:10192388

A; Ractus: preliminary

A; Rolecule type: DNA

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A,Residus: 1-759 <RBA
A,Cross-references: GB:AE002222; GB:AE002161; NID:G7189553; PIDN:AAF38461.1; PID:G718956
A;Experimental source: strain AR39; HL cells
       - Chlamydophila pneumoniae (strains CWL029 and AR
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Aypothetical protein CP0646 [imported] - Chlamydophila pneumoniae (strains C
2;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
2;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
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2; Mismatches 1; Indels
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MSS1_SCHPO YHA21_BIKCO PPCK_THEVO PD11_HUVAN RL28_STAAM CD3E_SHEBP RL24_SCHPO TINF4_MOUSE VIF_SIVSP V495_SYNY3 ALIGNMENTS	PRT; 711 786; Q16789; ed) sequence upda annotation up (Lactoferrin) xin C].	Craniata; Catarrhini	and; PubMed=2402455; K S.L., de Boer H.A., Pie ide sequence of human mam . 18:5288-5288(1990).	Engineering Research	EMBL/GenBank/DDBJ	, Richardson T. nence analysis o EMBL/GenBank/D	in coding and 5' £	l.; ice analysis of human l the EMBL/GenBank/DDBJ	: EMBL/GenBank/DDBJ
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FEBS Lett. 142:107-110(1982).
SEQUENCE OF 3-711 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rintworth G.K., Lin P.-Y., Bagti S., Reddy M.K., Kanai A., Hotta Y.,
A. Gumsiyeh M.B., Lin P.-Y., Bagti S., Reddy M.K., Kanai A., Hotta Y.,
R. Bi Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
A. Hajtmancik J.F., Tang C.T.;
A. Hejtmancik J.F., Tang C.T.;
A. Familial subepithelial corneal amyloidosis (gelatinous drop-like corneal agricophy): exclusion of linkage to lactoferrin gene.";
A. Pamilial subepithelial corneal amyloidosis (gelatinous drop-like corneal agricophy): exclusion of linkage to lactoferrin gene.";
A. Pamilial subepithelial corneal amyloidosis (gelatinous drop-like corneal agricophy): exclusion of linkage to lactoferrin gene.";
A. Punction: Transferrins are iron binding transport proteins which corneal adversary and a the second of the second
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MEDINE=91166929; BubMed=136929;
Tani F., Tio K., Chiba, Y. Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker B.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
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                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
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PubMed=9873069;
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Submitted (MAR-1997) to the EMBL/Genbank/DDBJ databases.
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MEDLINE=90064528; PubMed=2585506;
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"Mol. Biol. 209:711-734(1989).
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Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
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Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil
Jolles P.;
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MEDLINB-82262043; PubMed-7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil
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MEDLINE-88001031; PubMed=3477300;
Rado T.A., Wei X., Benz B.J. Jr.;
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MEDLINE=85076667; PubMed=6510420;
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comparisons with other transferrins.";
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PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
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Haridas M., Anderson B.F., Baxer E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
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Pan 88 amino acid long C-terminal sequence of human
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"Nucleotide sequence of human lactoferrin cDNA.";
Nucleic Acids Res. 18:4013-4013 (1990).
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MEDLINE=99190892; PubMed=10089347;
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                                                IISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
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Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;

Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;

Submitted (JUN-1999) to the EMBL/Genbank/DDBJ databases.

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUBLIX BICARBONATE (BY SIMILARITY).

-!- SUBCHILLAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOWOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Cameludae; Camelus.
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Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
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EMBL; AF156879; AAF82241.1; --
HSSP; O77811; JB1X.
InterPro; IRN01156; Transferrin.
Pfam; PF04405; transferrin. 2.
PRINTE; PR00422; TRANSFERRIN.
SMART; SM00049; TRER; 2.
PROSITE; PS00206; TRANSFERRIN. 1; 2.
PROSITE; PS00206; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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                       Length 711;
                       Score 67; DB 1; Length 711 Pred. No. 0.0002; 1; Mismatches 0; Indels
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16-CT-2001 (Rel. 40, Last sequence update)
16-CT-2001 (Rel. 40, Last sequence update)
16-CT-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
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MEDLINE=94380047; PubMed=8093048;

MEDLINE=94380047; PubMed=8093048;

MEDLINE=94380047; PubMed=8093048;

MICHARCTERIZATION OF the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 syntemy group.'

Biochem. Biophys. Res. Commun. 203:1324-1332(1994).

I PUNCTION: TRANSPERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.

SUBUNIT: WONOMER (BY SIMILARITY).

SUBCELLULAR LOCATION: Secreted.
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Sukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea;
Bovidae, Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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| IRON 1 (BY SIMILARITY) |
| IRON 1 (BY SIMILARITY) |
| IRON 1 (BY SIMILARITY) |
| IRON 2 (BY SIMILARITY) |
| IRON 3 (BY SIMILARITY) |
| IRON 4 (BY SIMILARITY) |
| ANION (BY SIMILARITY) |
| N-LINYED (GLUNAC . . ) (POTIN |
| N-LINYED (GLUN
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TISSUB-Mammary gland;
TISSUB-Mammary gland;
TISSUB-Mammary Gland;
Tubmitted (MPR-1996) to the EMBL/GenBank/DDBJ databases.
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TRFL HORSE
077811;
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                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                           EMBL; US3857; AAA97958.1; -.
EMBL; X78922; CAA55517.1; -.
EMBL; X78922; CAA55517.1; -.
EMBL; X78922; CAA55517.1; -.
InterPro; IPR001156; Transferrin, 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00494; TR FER, 2.
PROSTTE; PS00206; TRANSFERRIN.1; 2.
PROSTTE; PS00206; TRANSFERRIN.2; 2.
PROSTTE; PS00207; TRANSFERRIN.3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.4%; Score 50; DB 1; Length 708; 63.6%; Pred. No. 0.22; ive 3; Mismatches 1; Indels
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L -> R (IN REF. 2).
F -> R (IN REF. 2).
F -> P (IN REF. 2).
F -> P (IN REF. 2).
D -> G (IN REF. 2).
F2EDA3C83539960D CRC64;
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-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                             BY SIMILARITY.
LACTOTRANSFERRIN.
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Best Local Similarity
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708 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resolution.";
J. Mol. Biol. 289:303-317 (1999).

J. Mol. Biol. 289:303-317 (1999).

-I- FUNCTION TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-I- SUBGNIT: MONOMER.
-I- SUBCELLULAR LOCATION: Secreted.
-I- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-I- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ010930; CAA09407.1; -.

DR EMBL; AJ010930; CAA09407.1; -.

DR PDB; 1B1X; 02-PEB-99.

DR PDB; 1B70; 02-FEB-99.

DR PDB; 1B70; 02-FEB-99.

R PDB; 1B70; 02-FEB-99.

R PROSITE; PRO0405; TRANSFERRIN.

R SWART; SMO0094; TRANSFERRIN.

R PROSITE; PS00206; TRANSFERRIN.

R PROSITE; PS00206; TRANSFERRIN.

R PROSITE; PS00206; TRANSFERRIN.

R PROSITE; PS00207; TRANSFERRIN.

R PROSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P. "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Perissodactyla; Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Parinivasan A., Yadav M.P., Singh T.P.; Paramesivam M., Srinivasan A., Farbanasivam M., Subnit sequence of mare lactoferrin."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
PRT;
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MEDLINE=99296631; PubMed=10366507;
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MB4 / JCM 11007;

BIRDIINES-1992816; PubMed=11997336;
BAO (D., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

A complete sequence of T. tengcongensis genome.";

Genome Res. 12:669-700(22021.
                                                                                                                                                                                                                        (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                      59.2%; Score 42; DB 1; Length 695; 58.3%; Pred. No. 5.7; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales;
Thermoanaerobacteriaceae, Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.7%; Score 41; DB 1; Length 62; 70.0%; Pred. No. 0.69;
                                                                                                                                                                                                                                                                07BB84D50E1B165D CRC64;
                                                                               IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC. .) (F.
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Ribosomal protein, Complete proteome.
SEQUENCE 62 AA; 7037 MM; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L28.
RPMB OR TTE1495.
                                                                                                                                                                                                                                                                                                                                                                                                                                            62 AA
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Best Local Similarity 58.3
Matches 7; Conservative
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es 7; Conservative
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                                                                                                                                                                                                                                                                                                                                            1 CFQWKRNMRKVR 12
 NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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ID RL28_THETN
AC Q8R9Ū1;
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MEDLINE=92042099; PubMed=1939212;

Liu Y., Teng C.T.;

Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87280033; PubMed=3611056; Pentecost B.T., Teng C.T.; "Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Soiurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN.
1.
TREL MOUSE STANDARD; PRT; 707 AA. 198071; P70591; Q61799; Q92222; 1-402-1988 (Rel. 08, Created) 1-5-UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 1.
PROSITE; PS00205; TRANSFERRIN 2; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
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EMBL; D88810; BAA15633.1; -.
EMBL; EC06504; AAH06904.1; -.
EMBL; M74778; AA33427.1; -.
PIR; A28438; A28438.
HSSP; P02788; ICB6.
MGD; MGI:96837; Lrf.
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357
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                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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2; Mismatches

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Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda, Insecta, Perryota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
Abrill J.F., Agbayani A., An Andrews-Pfannkoof C., Baaldwin D.,
Bellew R.M., Bauu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLLED COLL (POTENTIAL).
MICROTUBLIA-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
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Pred. No. 92;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                      EMBL; U02963; AAA19956.1; -.
Interpro; IPR04273; Dynain heavy.
Pfan; PP03028; Dynein heavy; 1.
Motor proțein; Microtubules; Dynein; ATP-binding; Flagella;
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIA DROME STANDARD; PRT; 292 AA. 095ZIA: 097ZIA: 097ZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41./v,
Best Local Similarity 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||| : : | :: | 1852 CFQWQSQLRYIQ 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coiled coil
DOMAIN
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NP_BIND
NP_BIND
NP_BIND
SEQUENCE
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DOMAIN
DOMAIN
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NLA_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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J. Cell SCA. 107:635-644(1994).
J. Cell SCA. 107:655-644(1994).
-1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
DYNEIN HAS AFRARE ACTIVITY.
-1- SUBDNIT: CONSIGTS OF AT LEAST 3 HEAVY CHAINS (ALFHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitchell D.R., Brown K.S., "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MR -> IQG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 8.7;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MR -> 1QG (IN REF. 1).

R -> Q (IN REF. 2).

R -> L (IN REF. 2).

S -> T (IN REF. 2).

A -> D (IN REF. 2).

A -> D (IN REF. 1).

E -> G (IN REF. 1).

F -> G (IN REF. 1).

F -> G (IN REF. 1).
   2.
BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
0DA4 OR ODA-4 OR SUP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 4568 AA.
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STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629
77865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%;
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Best Local Similarity 54...
6; Conservative
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413
451
544
613
139
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707 AA;
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DISULFID
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       REPEAT
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BINDING
BINDING
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DYHB_CHLRE
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METAL
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-!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOWAL PROTEINS. PIR, A48396; A46396.
InterPro; IPR01383; Ribosomal L28.
Pfam; PF00830; Ribosomal L28; 1.
TIGRFAMS; TIGR00009; L28; 1.
Ribosomal protein.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, ALS91981; CAC99894.1; -. EMBL, ALS96170; CAC97160.1; -. Listilist; LIN0130; -. Listilist; LMO01816; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                   53.5%;
                                                                                                                                                                                                                                                                                                             Construction Similarity 66.70,
Best Local Similarity 66.70,
Best Active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeria monocytogenes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50S ribosomal protein L28. RPMB OR LMO1816 OR LIN1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1639, 1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 WKANLOKVR 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISMO
                                                                                                                                                                                                                                                                          SEQUENCE
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RESULT 10
RI28 LISENO
DT 115-UUN
DE 5508 rij
RESTEREN
ON NUBLTR
RA GAUGHER
RA DOMANN
RA DOMANN
RA DOMANN
RA DOMANN
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RA GAUG
                           SER RESERVED
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

R. Cherry J.M., Cawley S., Dahlke C., Davanport L.B., Davies P.,

R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

R. Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

R. Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

R. Harris N.L., Harvarov D., Helman T.J., Hernandez J.F., Houck J.,

R. Harris N.L., Harvarov D., Helman T.J., Hernandez J.F., Houck J.,

R. Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

R. Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

R. Jalali M., Maltei B., McIntosh T.C., McLeod M.P., Mosherson D.,

R. Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

R. Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

R. Markulov G., Milshina N.V., Mobarry C., Morris J., Mosheria A.,

R. Merkulov G., Milshina N.V., Muzphy L., Muzny D.M., Nelson D.,

R. Nelson D.R., Nalson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,

R. Rahnert K., Remington K.A., Nixon K., Nusskern D.R., Pecleb J.M.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

R. Spier E., Spradling A.C., Stapleton M., Skupski M.P., Yang S.,

R. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

R. Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho X., Smith H.O.,

R. Scheng X.H., Myers B.W., Rubin G.M., Venter E., Scheng L.,

R. Scheng X.H., Worley R., Zhou X., Zhu S., Zhu X., Smith H.O.,

R. Scheng X.H., Woodage T., Worley K.C., Wu C., Scheng L.,

R. Scheng X.H., Woodage T., Worley K.C., Wu C.,

R. Scheng X.H., Woodage T., Worley K.C., Wu C.,

R. Scheng X.H., Worley K.C., Wu C.,

R. Scheng X.H., Woodage T., Worley K.C., Wu C.,

R. Scheng X.H., Worley K.C., Wu C.,

R. Scheng X.H., Wo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92075758; PubMed=1742360; Kruft V., Kapp U., Wittmann-Liebold B.; Characterataation and primary structure of proteins L28, L33 and L34 from Bacillus stearchhemophilus ribosomes."; Biochimie 73:855-860(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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1- FUNCTION: REQUIRED FOR ELONGATION OF METOSIS I SPINDLE.
1- SIMILARITY: BELONGS TO THE DSCRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.9%; Score 39; DB 1; Length 292; 54.5%; Pred. No. 7.9; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0026629; nla.
SEQUENCE 292 AA; 31423 MW; 64FlBBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Bacillales, Geobacillus, NCBI_TaxID=1422,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF147700; AAD33987.1; -.
EMBL; AE003712; AAF55285.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribosomal protein L28.
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Best Local Similarity
6, Conserve
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Glaser P., Frangeul L., Bucker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dushout F.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dusurget O.,
Entian K.-D., Fshii H., Garcia-del Portillo F., Garrido P.,
Gautier L., Geobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Mattournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordaise G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Maquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
Science 294:849-852[2001).
L. Science 294:884-852[2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                        Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=L.monocytogenes, and L.innocua;
STRAIN=EGD-e / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; 1PR001383; Ribosomal L28.
Pfam; PF00830; Ribosomal L28; I.
TIGRRAMs; TIGR00009; L28; I.
Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 6991 MW; AA43DE039213C562 CRC64;
60 AA; 6810 MW; 2AD9161CD60E82F4 CRC64;
                                                                        Score 38; DB 1;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.5%; Score 38; DB 1; 66.7%; Pred. No. 2.3; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 41, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                         2; Mismatches
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                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIR-STCC 27343 / KID;
MEDLINE-STCC 27343 / KID;
MEDLINE-SOC59641: PubMed-7476192;
Bork P., Ouzounis C., Casari G., Schneider R., Sander C.,
Bolan M., Gillever P.M.;
"Exploring the Mycoplasma captricolum genome: a minimal cell reveals its physiology.";
Mol. Miscobloil 16:955-967(1995).
-!- SIMILARITY: BELONGS TO THE COF/YEHA/YIDA/YIGL (E.COLI) / YCSE/YXEH (B.SUBTILIS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simian immunodeficiency virus (F236/smH4 isolate) (sooty mangabey). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "An African primate lentivirus (SIVsm) closely related to HIV-2.";
Nature 339:389-392(1989).
-!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.5%; Score 38; DB 1; Length 267; 58.3%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=89262053; PubMed=2786147;
Hirsch V.M., Olmstead R.A., Murphey-Corb M., Purcell R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AA; 30425 MW; D5912DD5B39A8451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Virion infectivity factor (SOR protein) (Q protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z33006; CAA83689.1; -.
InterPro; IPRO01454; Hygnase/hydriase.
InterPro; IPR001150; Hygothet_cof.
Fam; PR00702; Hydrolase; 1.
PROSITE; PS01228; COF_1; 1.
Hygothetical protein...
NON_TER 267
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InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X14307, CAA32484.1; -.
PIR, S07989; S07989.
HIV; X14307; VIF$SMMH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 56...
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 CFGKKENMRQMR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWKRNMRKVR 12
NCBI_TaxID=2095;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpoBC operon.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Planet P., Jagoueix S., Bove J.M., Garnier M.; "Jagoueix Greening "Detection and characterization of the African Citrus Greening Liberobacter by amplification, cloning and sequencing of the rplKAJL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {RNA}(N).
-!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
                                                                                                                                                                                                                                                                                                                                      Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfan, PP00562, RNA pol B. 1.
PROSITE, PS01166, RNA POL BETA, PARTIAL.
Transferase, Transcription, DNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
Hypothetical protein (Fragment).
Mycoplasma capricolum.
Macoplasma Pirmicutes; Mollicutes; Entomoplasmatales;
Entomoplasmataceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001572; RNA_pol_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U09675; AAA19557.1; -
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                                                                                                                                                         STANDARD;
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4 WKRNIMRKVR 12
                        29 WKANLQKVR 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Nelspruit;
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P41187;
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SEQUENCE
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P53661;
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Y125 MYCCA
DD Y125 MY
AC P53661,
DT 01-0CT-
OS MYCOPIO
OS MYCOPIO
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Matches
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RPOB_LIBAF
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Gaps

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3; Indels

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EMBL; X61704; CAA43873.1; -.
EMBL; X61705; CAA43874.1; -.
PIR; S16767; S16767.
PIR; S16771; HSSP; O19673; 1HSB.
MIM; 142800; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003006; 19 MHC.
InterPro; IPR003597; 19 c1.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC I; 1.
ProDom; PD000050; MHC I; 1.
SMART; SM00407; IGC1; 1.
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                                                       NCBI_TaxID=9606;
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1115
2007
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227
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      precursor.
HLA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                A*3401.
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TRANSMEM
DOMAIN
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DISULFID
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1834 HUMAN STANDARD; PRT; 365 AA.
P30453; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34 (A-10) alpha chain
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-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                 Score 37; DB 1; Length 214; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.1%; Score 37; DB 1; Length 783; 50.0%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BMB1; 235602; CAA84471.2; -.
WormPep; R13G10.2; CE25088.
InterPerc; IPR002937; Amino_oxidase.
Pfam; PF01593; Amino_oxidase; 1.
Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
Hypothetical, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                           Gardner A.E.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                    Durbin R.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                             214 AA; 25140 MW; 9BCE884EC454BF3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             783 AA; 88799 MW; 8D087E96464DC908 CRC64;
                                                                                                                                                                                                         IS-DEC-1998 (Rel. 37, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein R13G10.2 in chromosome III.
873G10.2.
                                                                                                                                                                                      783 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                      1; Mismatches
                                                                                                                                                                                      PRT;
Pfam; PF00559; V1f; 1.
PRINTS; PR00349; VIRIONINFPCT.
ProDom; PD000063; Viral_infect; 1.
                                                                 52.1%;
75.0%;
                                                                 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                               Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                170 OWRRINKK 177
                                                                                                            3 QWKRNMRK 10
                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                      CAEEL
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                                            SEQUENCE
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AC P30453,

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DT 16-OCT-

DE HLA C1:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYMID outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (A*3401/A*3402).
SEQUENCE FROM N.A. (A*3401/A*3402).
MEDINE=9323511; PubMed=8475492;
Madrigal U.A., Hildebrand W.H., Selich M.P., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
du Toit E.D., Parham P.;
"Structural diversity in the HLA-Al0 family of alleles: correlations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW 34 (A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                          [1] — SEQUENCE FROM N.A. (A*3401/A*3402).
SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=93056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Marrell R.W., du Tolt E.D., Parham P.;
Mistinctive HLA-A,B antigens of black populations formed by interrallelic conversion.";
J. Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MICROGLOBULIN).
-!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
(AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
Homo saziens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00290; IG MHC; 1.
MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
SIGNAL
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FTId=VAR 004379.

K -> N (IN A*3402).

FTId=VAR 004380.

K -> I (IN A*3402).

FTId=VAR 004381.
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BY SIMILARITY.
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								CRC64;
P -> S (IN A*3402).	/FTId=VAR 004382.	Q -> R (IN A*3402).	/FTIG=VAR 004383.	W -> L (IN A*3402).	/FIId=VAR 004384.	L -> I (IN A*3402).	/FTId=VAR 004385.	063BF63E6E6E01F6
								X.
129		138		180		312		41055
129		138		180		312		365 AA; 41055 MW;
VARIANT		VARIANT		VARIANT		VARIANT		SEQUENCE
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Query Match
 50.7%;
 Score 36;
 DB 1;
 Length 365;

 Best Local Similarity 66.7%;
 Pred. No. 34;
 Pred. No. 34;
 Indels

 Matches 6;
 Conservative 1;
 Indels
 Pred. No. 34;
 Indels

 Qy 4 WRNNRKVR 12
 Indels
 Indels
 Pred. No. 34;
 Indels

 Db 84 WDRNTRKVK 92
 Indels
 Indels
 Indels

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0; Gaps

Search completed: February 21, 2003, 07:51:39 Job time: 6.2093 secs

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Q9jjzs mus musculu Q9sjjzs mus musculu Q9255 chlamydia p Q6258 encephalito Q8srg3 encephalito Q8srg4 encephalito Q9084 human immun Q77855 human immun Q77855 human immun Q9ml2 cicer ariet Q6sml1 cicer ariet Q6srg4 horseradish Q8yp77 anabaens sp Q8rax2 homo aspien Q9f7y4 salmonella Q8f2a4 mus musculu Q8f53 hemerocalli Q9ztp0 cryza sativ Q9ztp0 cryza sativ Q25f11 helicobacte
                                                                                                                                                                                                     Q9xfx1 cicer ariet
Q9ftt0 oryza sativ
Q8s487 zea mays (m
O81437 arabidopsis
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Ogw1d5 drosophila
Ogfhig arabidopsis
                                                                                                                                                                           oryza sativ
                                                                                                                                                                                              P96223 mycobacteri
                                                                                                                                                                           Q9zrh8 oryza sati
Q9nus2 homo sapien
017549 caenorhabdi
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Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UCY5;
01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-JUN-2001 (TYEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R., Strausberg R., Strausberg R., Strausberg B., Studitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL, EC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                      711 AA
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017549
094JZS
092955
062862
08884
090884
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09XKDS
098ML1
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Q8YP77
Q8TAX2
Q9F7Y4
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Q9W1D5
Q9FHI9
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Q81653
Q9ZTP0
Q25611
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Q9FTT0
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710000 00011
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Matches 10, Conservative
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TISSUE=PROSTATE;
Lactotransferrin.
Query Match
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Q8TCD2
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Q9UCY5
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Q986a rhizobium 1
Q986a rhizobium 1
Q92rh8 rhizobium m
Q87f3 brucella me
Q82f6 salmonella
Q9063 human immun
Q94p1 sesamum ind
Q96m21 homo sapien
Q90m31 homo sapien
Q91m33 halobacteri
Q9109 rhizobium 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ostcd2 homo sapien
Osucy5 homo sapien
Ostr80 ovis aries
O93780 caenorhabdi
                                                           February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds (without alignments) 114.078 Million cell updates/sec
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       GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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O31090
Q8XSE2
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Q9UCY5
Q93T80
Q93T80
Q8E9U1
Q9EAU
Q92EH8
Q8Z462
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sp_fungi:*
sp_human:*
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sp_phage:*
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Gapop 10.0 , Gapext 0.5
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2: sp_bacteria:*
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Match Length DB
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanserobacteriales; Thermoanserobacteriacese; Thermoanserobacter.
NCBL_TaxID=119072;
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MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816;

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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21082930; PubMed=11214968;
Kanako T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
                                                                             "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 16; Length 62;
Pred. No. 3.6;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                        Match 63.4%; Score 45; DB 5; Length 275; Local Similarity 72.7%; Pred. No. 3.1; es 8; Conservative 1; Mismatches 2; Indels
                                                                                                       investigating biology;";
Science 282:20.20.018[1998].
EMBL; Z8198; CA20.3137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-007-2001 (TrEMBLrel. 18, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Pyridoxamine 5-phosphate oxidase.
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SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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70.08;
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Best Local Similarity 70.v
Tr Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribosomal protein L28. RPMB OR TTE1495.
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                                                                                                                                                                                                                                                                                                                                                     2 FOWKRINMRKVR 12
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SEQUENCE FROM N.A.
STRAIN=MAFF303099;
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SEQUENCE FROM N.A.
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Matches
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     SORFFFRX
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinee, Ovis.
                                                                                                                                                           "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                      ٥;
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  Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                            81.7%; Score 58; DB 4; Length 38; 90.9%; Pred. No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=5127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
HSCP, O77698; LCE2.
InterPro, IPRO01156; Transferrin.
Fran, FORO405; transferrin; 1.
SEQUENCE 33 AA; 3914 MM; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                               InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN3-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                 seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; lBKA.
                                                                       SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
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01-FEB-1997 (TrEMBLrel. 02,
01-AUG-1998 (TrEMBLrel. 07,
01-DEC-2001 (TrEMBLrel. 19,
F5314.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
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Matches 6; Conservative
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Matches 10; Conserv
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                            NCBI_TaxID=9606;
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         1 CFQWKRNMRKVR 12
                                       88 CFHWKSLRROVR 99
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SEQUENCE FROM N.A.
STRAIN=1021;
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Best Local Similarity
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Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.,
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21608550; PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okurav V.K., Zhou Y., Chen L., Wood G.E., Almeida M.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R. Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Hourlo B., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Houmtel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Flanagan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., "Genome sequence of the plant pathogen and biotechnology agent Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nester E.W.; "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pyridoxamine 5'-phosphate oxidase.
Pyridoxamine 5'-phosphate oxidase.
PAGROBACTERIUM tumefaciëns (strain CS8 / ATCC 33970).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
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                                                                                                                                                                                                                       57.7%; Score 41; DB 16; Length 205; 58.3%; Pred. No. 12; tive 1; Mismatches 4; Indels
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                                                                                                                                                                                        205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
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                                                                          EMB1, AP003011, BAB53553.1; -.
InterPro, IRR000659; Pyridox oxidase.
Pfam, PP01243; Pyridox oxidase, 1.
ProDom; PD006312; Pyridox oxidase; 1.
TIGRFAMS; TIGR00558; pdxH; 1.
COMDITE; R01064; PYRIDOX_OXIDASE; 1.
SEQUENCE 205 AA; 23300 MW; 0BADE4CD3
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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MEDLINE=21608551; PubMed=11743194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 294:2317-2323(2001),
                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                Mesorhizobium loti.";
DNA Res.'7:331-338(2000)
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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NCBI_TaxID=176299;
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE 206 AA
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A capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
B Goistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Gottie T., Goffeau A., Rahn D., Kiss E., Lelaure V., Masuy D.,
A maiver C., Thebault P., Purhler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
Analysis of the chromosome sequence of the legume symbiont
T. Analysis of the chromosome sequence of the legume symbiont
T. Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
BMBL; AL591785; CAC45467.1;
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
Probom; PRO0659; Pyridox_oxidase.
Probom; PRO06512; Pyridox_oxidase; 1.
Probom; PRO1651; Pyridox_oxidase; 1.
Probom; PSO1064; PyRIDOX OXIDASE; UNKNOWN_1.
Oxidoreductase; Complete Protecome.
SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;
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SETALINE=16M / ATCC 21456 / BIOTYPE 1;
MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
                                                                            01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
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Brucellaceae, Brucella.
                                                                                                                                                               (EC 1.4.3.5).
PDXH OR R00895. OR SMC00069.
Rhizobium mellloti (Sinorhizobium mellloti).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (BC 1.4.3.5)
BMEIIS17.
Brucella melitensis.
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Pred. No. 12;
1; Mismatches 4
  206 AA
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                                            01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last seq 01-JUN-2002 (TrEMBLrel. 21, Last ann
PRT;
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Local Similarity 66.7
es 6; Conservative
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nes 6; Conserv
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SEQUENCE
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Q96M2.1
ID Q96M2.1
ID Q96M2.0
DT 01-DE
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain in Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Backer S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., Milte N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE009587; AAL52698.1; -
InterPro; IPRO0659; Pridox_oxidase.
Prom; Pr0143; Pridox oxidase; 1.
ProDom; PD006312; Pridox_oxidase; 1.
ProDom; PD006312; Pridox_oxidase; 1.
PROSTE; PS01064; PriLOX_OXIDASE; 1.
Oxidoreductase; Complete proteome.
SEQUENCE 208 AA; 23866 MW; CBIP50BC9612DBZ8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:848-852(2001).
EMBL, AL627276, CADOGA911, -.
Hypothetical protein; Complete proteome,
SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Glycoprotein gpl20 (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCbl_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 AA
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es 7; Conservative
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nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella.
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Q82462;
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Q8Z462
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STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
"Molecular cloning of 11S globulin and 2S albumin, the two major seed storage proteins in sesame.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2S albumin.
Sesamum indicum (Oriental sesame) (Gingelly).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
STRAIN=NUS182; Brandel W.K., Janssens W., Adu-Sarkodie Y., Apradyei E., Anyomi F., Aidoo S., Barnor J.S., Yamamoto N., Ishikawa K., Sata T., Kurata T.; "Genetic and phylogenetic analysis of HIV-1 strains from Southern
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.3%; Score 40; DB 15; Length 81; 66.7%; Pred. No. 7.1; tive 2; Mismatches 1; Indels
                                                                                                                                                                           Juneary (JAN-1998) to the EMBL/GenBank/DDBJ databases. Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AJ225659; CAA12541.1; -. Interprety, IRRODAT7; GP120. Pfam; PR00516; GP120; 1. AIDS; Coat protein; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                      81 81 81 81 82 81 843 81 84 9138 MW; 2D43DCD554295572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel, 12, Created)
01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-MAR-2002 (TrEMBLrel, 20, Last annotation update)
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Last annotation update)
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EMBL; AF091841; AAD42943.1; -.
InterPro; IPR0003612; Napin.
InterPro; IPR000617; Napin.
InterPro; IPR00017; Napin.
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01-DEC-2001 (TrEMBLrel. 19, Last seque
01-DEC-2001 (TrEMBLrel. 19, Last amon
CDNA FLJ22891 fis, clone TESTI2004929
Homo sapiens (Human).
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PRINTS; PR00496; NAPIN.
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MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MILLARIA H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Martzell S., Weiler K., Cruz R., Melli R., Goo Y.A.,
Leithauser B., Kreller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
A leamyer T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
A lam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
M. Bhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
T. Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
M. BMBL; ABO01046; Speptide repeat.
InterPro: IPR001646; Speptide repeat.
InterPro: IPR001622; K-channel_pore.
Rian; PR00805; Pentapeptide; Z.
W. Complete Proteomentapeptide; Z.
W. Complete Proteomentapeptide; Z.
W. Complete Proteomentapeptide; Z.
                                                                                                   SEQUENCE FROM N.A.
TISSUGATESTIS;
Oshima A., Takahashi-Pujii A., Tanase T., Imose N., Takeuchi K.,
Oshima A., Takahashi-Pujii A., Tanase T., Imose N., Takeuchi K.,
Atita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Satio K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Skyine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
NIBO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKOS7453; BAB71493.1; --
SEQUENCE 274 AA; 30083 MW; IDD43654D4135B2F CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 56.3%; Score 40; DB 4; Length 274; Local Similarity 50.0%; Pred. No. 25; 3; Indels is 6; Conservative 3; Mismatches 3; Indels
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Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         584 AA; 65151 MW; 21BF5D5F0486CCC6 CRC64;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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                                                    NCBI_TaxID=9606;
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DT 01-JAN-1998 (TERMBITE). 05, Created)
DT 01-JAN-1998 (TERMBITE). 05, Last sequence update)
DT 01-OCT-2001 (TERMBITE). 18, Last sequence update)
DS Rhizolum leguminosarum (biovar viciae).
OC Rhizolum leguminosarum V.N.;
RN I1]
RN SEQUENCE FROM N.A.
RN I2]
RN I2]
RN I2]
RN I2]
RN KSEQUENCE FROM N.A.
RN I28hina T.V., Kanapin A.A., Shlyapnikov M.G.,
RN KSEQUENCE FROM N.A.
RN KSEQUENCE FROM N.A.
RN MEDLINE=99113394; PubMed=9914965;
RN KSEQUENCE FROM N.A.
RN HYPOTHETICAL PROCESSIO: ALSO SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;
CHERY MATCHES 6:08; Pred. No. 37;
MATCHES 6; Conservative 3; Mismatches 1; Indels 0; Gaps
ON 3 OWNENDARIENTE 254
DD 245 RWIRNLERE 254
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Search completed: February 21, 2003, 08:00:45 Job time : 22.6744 secs

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WPI; 2000-147388/13.
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| SIDS2/gcgdata/geneseq_geneseq_embl/AA1990.DAT:
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1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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## ALIGNMENTS

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Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolphin GT;
                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:93.
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AAY78093 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                    Homo sapiens.
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29-DEC-1998;
                                                                                  25-APR-2000
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                                                                                                                                                                                                                                                                                                      Synthetic.
                                         AAY78093;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferin. The peptides are taken up in the intestine through binding to specific lactoferin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary trget infections, collitis, and candida infections (such as urinary trget infections, collitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have dealred anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used alinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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             New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lactoferrin derived peptide SEQ ID NO:74.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78074 standard; Peptide; 12 AA.
                                                                      Claim 22; Page 38; 102pp; English.
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Best Local Similarity
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29-DEC-1998;
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Dolphin GT

Baltzer L,

Mattsby-Baltzer I,

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                            Length 12;
                                                                                                                                                                                                                                                                                                        Score 65, DB 21; Length 12
Pred. No. 0.00019;
1; Mismatches 0; Indels
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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                              AAY78092 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 38; 102pp; English
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98SE-0002562.
98SE-0004614.
                                                                                          Query Match 91.3%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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17-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                Score 63, DB 21, Length 12, Pred. No. 0.00042;
0, Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:92.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to especific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urihary tract infections, colitis, and Candida infections (such as uncosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used as preservatives. The peptides are also can though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used all initially on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
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Pred. No. 0.0009;
1; Mismatches 1; Indels
Score 63; DB 21; Length 12;
Pred. No. 0.00042;
0; Mismatches 1; Indels
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ilarity 83.3%;
Conservative
      Query Match 91.3%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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98SE-0002562.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                              1 CFOWKRAMRKVR 12
                                                                                                                                                                                        1 CFOWKRNMRKVR 12
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Best Local Similarity
Matches 10; Conserv
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29-DEC-1998;
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                      Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                Human lactoferrin derived peptide SEQ ID NO:86.
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AAY78086 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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                                                                            25-APR-2000 (first entry)
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Best Local Similarity 83.3
Matches 10; Conservative
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29-DEC-1998;
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                                                                                                                                                                                                                                                                        Synthetic.
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                                      AAY78086;
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                                                                                                                                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; collitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dolphin GT;
                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                   AAY78090 standard; Peptide; 12 AA.
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98SE-0002562.
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                     1 CFQWQRXMRKVR 12
1 CFOWKRAMRKVR 12
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Best Local Similarity
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17-JUL-1998;
29-DEC-1998;
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ANY9801 to AAY98100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrans), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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83.3%; Pred. No. 0.0013;
tive 1; Mismatches 1; Indels
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Matches

RESULT 7 AAY78086

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infections (such as unibrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungacidal and bactericidal and may also be used as preservatives.

Byon though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would costs. Therefore, provision of peptides based on lactoferrin at lower
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Best Local Similarity 83.3%;
Matches 10; Conservative 1
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29-DEC-1998;
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Dolphin GT;

Baltzer L,

98SE-0002441. 98SE-0002562 98SE-0004614

99WO-SE01230

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the direction. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections and/or prevention of infections (such as urinary tract infections and/or tumours. The peptides can also be used on the form and or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also thungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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0
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formula food
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Pred. No. 0.002;
1; Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                         13-JAN-2000
   Synthetic.
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0; Gaps

Score 59; DB 21; Length 12; Pred. No. 0.002; 1; Mismatches 1; Indels

(first entry)

Baltzer L,

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Human lactoferrin derived peptide SEQ ID NO:84.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78084 standard; Peptide; 12 AA
                                                                                                                            Claim 18; Page 73; 102pp; English
                                                           Hanson LA, Mattsby-Baltzer I,
06-JUL-1998; 98SE-0002441.
17-JUL-1998; 98SE-0002562.
29-DEC-1998; 98SE-0004614.
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Best Local Similarity 83.3
Matches 10, Conservative
                                      (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                    1 CFOWKRAMRKVR 12
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12 AA;

98SE-0002562. 98SE-0004614.

99WO-SE01230, 98SE-0002441

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the lactoferrin receptors and are then transported binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as unimary tract infections, colitis, and candida infections (such as unimary tract infections, colitis, and candida infections on a musosal mebrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, lactoferrin, modification, infection; inflammation, tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.5%; Score 59; DB 21; Length 12; 83.3%; Pred. No. 0.002;
Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:95.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
  Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78095 standard; Peptide; 12 AA.
                                                                                                                                                                Claim 22; Page 36; 102pp; English.
  Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 AA;
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
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                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Claim 22; Page 38; 102pp; English.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections. colitis, and candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. Infode such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.5%;
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98SE-0002562.
98SE-0004614.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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Gaps ö

DB 21; Length 12; 0.002; 1; Indels

Score 59; DB 2 Pred. No. 0.002 1; Mismatches

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as

Dolphin GT

Baltzer L,

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production
            membrane), inflammations add/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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  colitis, and Candida infection on
                                                                                                                                                                                                                                                85.5%; Score 59; DB 21; Length 13; 83.3%; Pred. No. 0.0021;
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                                                                                                                                                                                                                                                                                      1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78048 standard; Peptide; 13 AA.
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98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                  Local Similarity 83.3
ses 10; Conservative
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                                                                                                                                                                                                             13 AA;
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29-DEC-1998;
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Matches
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract inflammations and/or prevention of infections (such as uninary tract inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumo
urinary tract infection; colitie; Candida infection; fungicidal;
bactericidal; preservative.
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98SE-0002562.
98SE-0004614.
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                                                                                                                      13 AA;
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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                                                                                                                      Sequence
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AAY78049
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99WO-SE01230.

Dolphin GT;

Baltzer L,

85.5%; Score 59; DB 21; Length 13;

Query Match

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83.3%; Pred. No. 0.0021;
tive 1; Mismatches 1; Indels
Best Local Similarity 83.3
Matches 10; Conservative
                                                                             1 CFOWKRAMRKVR 12
                                                                                                           2 CFOWORNMRKVR 13
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0
                                                                                                                                                                                                            Gaps
costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                            ö
                                                                                                                                                  Query Match 85.5%; Score 59; DB 21; Length 13; Best Local Similarity 83.3%; Pred. No. 0.0021; Matches 10; Conservative 1; Mismatches 1; Indels
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Search completed: February 21, 2003, 07:56:44 Job time : 28.093 secs

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Sequence 2
Sequence 2
Sequence 2
Sequence 2
Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAMAMOTO, NACKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHICBAKI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: VINDANTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATERY ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
LOCATION: 1..16
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BOSTON

STATE MA

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC COMPALINE

COMPUTER: Patentin Release #1.0, Version #1.25

SUFFWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204,487

FILING DATE: 02-MAR-1994

CLIASSIPICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, PAULA A.

REFERENCE/DOCKET NUMBER: PJN-019

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 3:

SEQUIENCE CHARACTERISTICS:

SEQUIENCE CHARACTERISTICS:
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
 RESULT 1
US-08-204-487-3
 Sequence 8, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 24, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 26, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
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                                                                                               February 21, 2003, 07:50:40; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
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Sequence 8, A
Sequence 8, A
Sequence 30,
Sequence 29,
Sequence 6, A
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Sequence 7,
Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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(GGTZ 6/ptodata/1/iaa/5A_COMB.pep:*

(GGTZ 6/ptodata/1/iaa/6B_COMB.pep:*

(GGTZ 6/ptodata/1/iaa/6A_COMB.pep:*

(GGTZ 6/ptodata/1/iaa/6B_COMB.pep:*

(GGTZ 6/ptodata/1/iaa/6B_COMB.pep:*

(GGTZ 6/ptodata/1/iaa/PCTUS_COMB.pep:*

(GGTZ 6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-628-948-8

US-07-755-161A-3

US-07-755-161A-3

US-07-811-174-3

US-08-26-711-25

US-08-26-771-25

US-08-26-771-25

US-08-26-771-25

US-08-26-771-25

US-08-26-771-25

US-08-381-984-24

US-08-381-984-24

US-08-381-984-24

US-08-381-174-10

US-07-55-161A-8

US-07-755-161A-8

US-08-266-771-39
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                                                                                                                                                                                                                                                                    262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                         ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                         US-09-743-107B-93
69
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Match Length
                                                                                                                                                           itle:
erfect score:
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                                                                      M protein
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                                                                                                    no un
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RESULT 4
US-08-475-055-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: YOUR MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 0.0015;
1; Mismatches 1; Indels
                                                                                                 Query Match 85.5%; Score 59; DB 1; Length 18; Best Local Similarity 83.3%; Pred. No. 0.0015; Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 411 Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: Usw Jersey
COUNTRY: Usw Jersey
COUNTRY: Usw Jersey
CONFUTER: EBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
CCLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
CCLASSIFICATION: 436
CCLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: JGASSOFICATION: 67,42
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-580
TELEPHONE: 201 487-580
TELEPHONE: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TUNE APPLICATION: ACID ACID ACIDS
TELENCE: AMINO ACIDE ACIDS
TELENCE: AMINO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-08-485-948-8; Sequence 8 Application US/08485948; Sequence 8. Patent No. 585582; GENERAL INFORMATION:
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLCGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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CFOWORNMRKVR 12

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| Section 6 | Application US/08628380|
| Patent No. 2801341|
| Garraba. Introduction US/08628380|
| Application 10 | Application US/08628380| |
| Application 11 | Application US/0862830|
| Application 12 | Application US/086283|
| Application 20 | Application Section 12 | Application Section 13 |
| Application 20 | Application Section 3 | Application Section 3 |
| CONTRIET OF SECTION SECTI
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
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OPERATING SYSTEM: FLG. LO.
SOFTWARE: DisplayMarite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 33,
APPLICATION NUMBER: 33,367
RATIONEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,267
REFERENCE/DOCKET NUMBER: 33,267
REFERENCE/DOCKET NUMBER: 33,267
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOCUMENT NUMBER:
FILING DATE:
PRELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
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NAME/KEY: modified site
LOCATION: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-755-161A-3
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Pred. No. 0.0015;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/07755161A
Patent No: 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                          ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION
RPLICATION NUMBER: 08/486,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/486,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/48,217
FILING DATE: APRIL 7, 1995
CLASSIFICATION NUMBER: 08/418,642
FILING DATE: ADVID 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: ADVID 7, 1995
TILING DATE: ADVID 7, 1
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MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201343-1684
FELEX: 133521
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE: internal
S-08-475-055-8
        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQRNMRKVR 12
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LOCATION: 2
IDENTIFICATION WETHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 19
OTHER INFORMATION: Oys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
AUTHORS.
AUTHORS:
AUTHORS:
AUTHORS:
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APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NOSUCHIT, WATARU
APPLICANT: MOSUCHIT, WATARU
APPLICANT: TONAKA, SHIGEAKI
APPLICANT: TAWASAKI, SOSHIHIRO
APPLICANT: TAWASAKI, YOSHIHIRO
APPLICANT: TAWASAKI, YOSHIHIRO
APPLICANT: TONENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: MOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INPORMATION:
NAME: CAMPBELL, PAULA A.
RECISTRATION NUMBER: 32,503
RECISTRATION NUMBER: 93,503
TELECOMMINICATION INPORMATION:
TELECOMMINICATION INPORMATION:
TELECOMMINICATION INPORMATION:
TELECOMMINICATION INPORMATION:
TELECOMMINICATION INPORMATION:
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Best Local Similarity 83.3%; Pred. No. 0.0016;
Matches 10; Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWKRAMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-891-174-3
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                                                              Gaps
                                                              1; Indels
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Patent No. 5317084

Patent No. 517084

Patent No. 517084

Patent No. 517084

Patent No. 517084

APPLICANT: Mamoru TCMITA et al.

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10

CONTESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700

CITY: Weathington STREET: B.C.

COMPURSY: U.S.A.

ZIP: 2006

COMPURSY: U.S.A.

MEDIUM TYPE: Diskette, 5.25 inch, 500KD

COMPURSY: LEM Compatible

COMPUTER: IEM Compatible

COMPUTER: LEM Compatible

COMPUTER: Diskette, 5.25 inch, 500KD

COMPUTER: USA, 5.25 inch, 500KD

COMPUTER: Diskette, 5.25 inch, 500KD

COMPUTER: Di
                   83.3%; Pred. No. 0.0016;
                                                         1; Mismatches
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified site
              Best Local Similarity 83.3
Matches 10; Conservative
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHRONOSOME/SEGMENT:
MAP POSITION:
UNITE:
PRAFIT:
PRAFIT
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                    1 CFQWKRAMRKVR 12
                                                                                                                                                                                                        2 CFOWORNMRKVR 13
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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Gaps

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RESULT 9

US-08-256-771-25

US-08-256-771-25

US-08-256-771-25

Sequence 25, Application US/09256771

Patent No. 565631

SHORMAND THORAMATION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING TITLE OF INVENTION: PRODUCTS THEREWITH NUMBER OF ENGURNES: ADDRESS: ADDRESSE: Wanderch, Lind & Ponack STRET: D.C.

ZIPIETE: D.C.

ZIPIETE: D.C.

ZIPIETE: D.C.

CONDUTER: BLO COMPATIBLE FORM: Machington STATE: D.C.

SOFTWARE: Wachington No-DOS

SOFTWARE: Wachington No-DOS

SOFTWARE: Wachington DATA: APPLICATION NUMBER: US/08/256,771

FILING DATE: TILING DATE: APPLICATION NUMBER: 33,367

REGISTRATION NUMBER: 33,367

REGISTRATION INFORMATION: TELECOMMUNICATION INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 1; Length 20; Pred. No. 0.0016;
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                                                                                                                        1; Mismatches
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                                                               85.5%;
83.3%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                               Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                    1 CFOWKRAMRKVR 12
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      US-08-256-771-24
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US-08-381-984-24
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Patent No. 565691

GRERAL INFORMATION:
APPLICANT: MAMORY TOMITA et al.
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
CITY: Washington
CITY: Washington
CITY: Diskert, 5.25 inch, 500 kb
MEDIUM TYPE: Diskert, 5.25 inch, 500 kb
COMPUTER EDADALE FORM:
MEDIUM TYPE: Diskert, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: US.A.
APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.5%; Score 59; DB 1; Length 20; Best Local Similarity 83.3%; Pred. No. 0.0016; Matches 10; Conservative 1; Mismatches 1; Indels
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LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                                                                   LOCATION: 1.70
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
S-08-204-487-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDENNES: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
AUNUS: WAREN W. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWKRAMRKVR 12
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S-08-256-771-24
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Gaps

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Sequence 4, Application US/09508734

Sequence 4, Application US/09508734

Sequence 4, Application US/09508734

Sequence 4, Application US/09508734

GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Wase production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: USEGIL microorganism thereof
TITLE OF INVENTION: UNMBER: US/05/0508,734

CURRENT APPLICATION NUMBER: DCT/KR99/00373

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1998-07-13

NUMBER: OF SEQ ID NOS: 12

SOTTWARE: Kpatentin 1.71

SEQ ID NO 4
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DEBNIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.0016;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                              ZIP: 2005
ZUP: 2
                                                                                                                          STREET: 805 Fifteenth Street, N.W., #700
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Best Local Similarity 83.3%;
Matches 10; Conservative
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWKRAMRKVR 12
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                                                                                                                                                             Washington
                                                                                                                                                                                             D.C.
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US-09-508-734-4
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NAME/KSY:
LOCATION:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
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LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.5%; Score 59; DB 1; Length 20; 83.3%; Pred. No. 0.0016; ive 1; Mismatches 1; Indels
; Sequence 24, Application US/08381984;
; Patent No. 5804555;
; GENERAL INFORMATION:
; TATLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: washington
STATE: D.C.
COUNTER U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER ACUCA

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: Diskette, 3.5 inch, 1.44 mb

COMPUTER: Diskette, 3.5 inch, 1.44 mb

COMPUTER: DISK COMPACIBLE

COMPUTER: Mordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/381,984

FILING DATE: April 11, 1995

CLASSIFICATION 252

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY AGENT INFORMATION:

NAME: WARTEN M. Cheek, Jr.

REGISTRATION NUMBER:

REGISTRATION NUMBER:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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Patent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conservat
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US-08-381-984-25
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HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CRONDS OUNCE:
LIBERRY:
CLONE:
CHRONOSOME/SEGNENT:
MAP POSITION:
UNITS:
FEATURE:
NAMMYKEY: modified site
LOCATION:
CTHER INFORMATION: /note= "thiol group of orther INFORMATION: /note= "thiol group of orther INFORMATION: /note= "thiol group of orther INFORMATION: /note= "thiol group of cys residue at location 21"
FRANTE:
NAMMYKEY: modified site
LOCATION: 21
LOCATION: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: //note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" PUBLICATION INFORMATION:
AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
PUBLICATION DATE:
RELVANT RESIDUES IN SEQ ID NO:
02-07-755-161A-10
PILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. CHEEK JT.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECPHONE: 202-371-8856
TELEFYX: 202-371-8856
TELEFX: 202-371-8856
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 21 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                           TYPE: AMINO ACID
STRANDEDNESS: $1ng
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENEE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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                                                                                                                                                                                                                                                        35ULT 13
3-09-508-734-6
Sequence 6, Application US/09508734
Patent No. 64.23509
GENERAL INFORMATION:
PAPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: Useful microorganism thereof
TITLE OF INVENTION: Useful microorganism thereof
CURRENT PAPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 1999-07-14
PRIOR PAPLICATION NUMBER: PCT/KR99/00373
PRIOR PAPLICATION NUMBER: KR1998-29351
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR PILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: KopatentIn 1.71
SEQ ID NO 6
LBINGHIS 24
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                                                                                                  85.5%; Score 59; DB 4; Length 22; 83.3%; Pred. No. 0.0018;
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                                                                                                                                       1; Mismatches
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Matches 10; Conservative
                                                                                                                                       10; Conservative
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                           TYPE: PRT
ORGANISM: Homo sapiens
5-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
3-09-508-734-6
                                                                                                                                                                        1 CFOWKRAMRKVR 12
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Best Local Similarity
Matches 10; Conserv
             LENGTH: 22
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IDENTIFICATION METHOD: OF Thiol group of OTHER INFORMATION: (A) of E = "thiol group of OTHER INFORMATION: (A) of E = "thiol group of OTHER INFORMATION: CYS residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21"
NAME/KEY: modified site
LOCATION: 21
                                            Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICATE MAGNOTU TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCES. 11
CORRESPONDENCES. 12
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
GITT: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                 CITY: WASHLINGLOIL
STATE: D.C.
ZIP: D.C.
ZIP: 20005
ZIP: 20005
ZIP: 20005
ZIP: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: DISACTE, 5.25 inch, 500Kb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARRE: DISPLAYMYLICE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/755,161
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. CHECK JT:
REGISTRATION NUMBER: 33,367
RETERRENGE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acida TYPE: amino acida STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: modified site
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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MMEDIATE SOURCE:
LIBRARY:
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ORIGINAL SOURCE:
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MOLECULE TYPE:
HYPOTHETICAL:
ESULT 15
IS-07-891-174-10
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us-09-743-107b-93.rapb

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Sequence 132, App
Sequence 14, App
Sequence 16, App
Sequence 117, App
Sequence 118, App
Sequence 118, App
Sequence 118, App
Sequence 118, App
Sequence 146, App
Sequence 466, App
Sequence 416, App
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Pred. No. 0.00047;
1; Mismatches 1; Indels
3 9 US-10-028-072-132
3 9 US-10-121-049-132
3 9 US-110-123-904-132
3 9 US-110-140-470-132
3 9 US-110-140-470-132
3 9 US-110-175-746-132
3 9 US-110-175-746-132
3 9 US-110-176-918-132
3 9 US-10-176-918-132
3 9 US-10-176-918-132
3 0 US-09-764-864-1346
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5 US-09-764-864-1346
5 US-09-764-864-1346
5 US-09-764-867-12
5 US-09-764-867-12
5 US-09-764-867-13
6 US-09-764-867-13
7 US-09-778-122A-466
7 US-09-778-122A-466
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-198-80-80-1

SQUENCE 2, Application US/09798869

Publication No. US2003002281A1

GENERAL INFORMATION:

APPLICANT: UCHN SIGURD SVENDSEN

APPLICANT: (YSTEIN REXDAL

APPLICANT: LARS VORLAND

APPLICANT: LARS VORLAND

APPLICANT: AA-049-PCT-USA-A

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: PCT/GB99/02851

PRIOR PILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR PILING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SSOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NO :

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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APPLICANT: JOHN SIGURE SVENDSEN; APPLICANT: (YSTEIN REKDAL); APPLICANT: BALDUR SVEINBJ(RNSSON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.5%;
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CORGANISM: HOMO SAPIENS
US-09-798-869-2
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       10;
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US-09-798-869-20
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US-09-798-869-2
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Best Local Si
Matches 10;
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Sequence 2, Appli
Sequence 3, Appli
Sequence 23, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 22, Appli
Sequence 8, Appli
Sequence 29, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 511, Appli
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Sequence 2, Appl
Sequence 42, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                     February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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Sequence 20,
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                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PUSOB NEW PUB.pep:*
3: \cgn2_6/ptodata/2/pubpaa/PUSOB NEW PUB.pep:*
4: \cgn2_6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
5: \cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
6: \cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
7: \cgn2_6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
8: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
9: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
11: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
12: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
13: \cgn2_6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
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14: \cgn2_6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
14: \cgn2_6/ptodata/2/pubpaa/USO0 PUBCOMB.pep:*
                       GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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US-09-798-869-2
US-10-02-09-869-2
US-09-798-869-3
US-09-798-869-3
US-09-798-869-4
US-09-798-869-4
US-09-798-869-4
US-09-798-869-4
US-09-798-869-4
US-09-798-869-8
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US-10-042-417-42
                                                                                                                                                                                                                                                                                        otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            156504 seqs, 31069816 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Gaps

Gaps

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OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens OTHER INFORMATION: sequence)
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Score 59; DB 9; Length 694;
Pred. No. 0.019;
1; Mismatches 1; Indels
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Pred. No. 0.01;
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Pred. No. 0.022;
                                                                                                                                                                                                                                  APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYBINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE FEPTIDES
FILE REFERENCE: AJ4049-FCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-36
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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Publication No. US20030022821A1
GENERAL INFORMATION:
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63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
     Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                      1 CFOWKRAMRKVR 12
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Best Local Similarity
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; ORGANISM: CAPRINE
US-09-798-869-3
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US-09-798-869-3
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Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kruzeki, Tomasz
APPLICANT: Kurecki, Tomasz
APPLICANT: Doyle, Darrell D.
APPLICANT: Doyle, Darrell D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES:
AUMBER OF SEQUENCES:
ADDRESSER: Jacobson, Price, Holman & Stern.
                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                  Length 25;
                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                  Score 59; DB 9; I
Pred. No. 0.00078;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Jacobson, Price, Holman & Stern STRET: 400 Seventh St. N.W.
COLIY: Washington D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TILLE OF INVENTION: BIOACTIVE PEPTIDES
TILLE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-8
NUMBER OF SEQ ID NOS: 30
SOFWARE: FRANCE FILING DATE: 1998-09-8
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 694 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                   , ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                           3 CFOWORNMRKVR 14
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Pred. No. 1.2;
2; Mismatches
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APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/08/97
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 22
                                                                                                                         US-00-798-869-4

Sequence 4, Application US/09798869

Publication No. US20030022821A1

GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SYENDSEN

APPLICANT: JOHN SIGNED SYENDSEN

APPLICANT: JARS VORLAND

TILLE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION: BIOACTIVE PEPTIDES

TILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT PILING DATE: 2001-02-27

PRIOR PLILCATION NUMBER: BCT/GB99/02851

PRIOR PLILCATION NUMBER: GB9818938.4

PRIOR PLILNG DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FSELSEQ for Windows Version 4.0
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Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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1 CFOWKRAMRKV 11
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: MURINE
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llarity 54.5%; Pred. No. 0.49;
Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.0%; Score 49; DB 9; Length 25; 63.6%; Pred. No. 0.037;
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1; Indels
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Publication No. US20030022821A1

GENERAL INFORMATION:
APPLICANT: OWN SIGHED SYBNDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: APPLICANT: DALUNE SYBINBJ (RNSSCN)
APPLICANT: LARS VORLAND
TITLE OP INVENTION: BIOACTIVE PEPTIDES
FILE REFERRENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB918938-4
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FSELSEQ for Windows Version 4.0
SEQ ID NO 7
LUNGTH: 15
Mismatches
                                                                                                                                                                                          Sequence 23, Application US/09798869
Publication No. US20030022821A1
APPLICANT: ON. US20030022821A1
APPLICANT: JOHN SIGHED SVENDSEN
APPLICANT: ALDUR SVEINDS UNSEND
TITLE OF INVENTION: BIOACTUR PEPTIDES
TILE OF INVENTION: BIOACTUR PEPTIDES
TILE OF INVENTION: BIOACTUR PEPTIDES
CURRENT FILING DATE: 201-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastERQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 25
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ORGANISM: Artificial Sequence
7; Conservative
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Best Local Similarity
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                                           1 CFQWKRAMRKV 11
                                                                                      3 CYQWQRRMRKL 13
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Best Local Similarity
Matches 6; Conserv
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ORGANISM: CAPRINE
3-09-798-869-23
Matches
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; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                    APPLICANT: Pear, Sharron G.
APPLICANT: Harris, Pear, Sharron G.
APPLICANT: Harris, David K.
APPLICANTION: Harris Expression Analysis BY MICROARRAY
CURRENT APPLICATION NODER: US/09/864,761

PRIOR FILING DATE: 2000-09-36

PRIOR FILING DATE: 2001-09-36

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 20
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXT_HUMAN HIT: AW294800.1, EVALUE 1.00e-06
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                                                                      Sequence 47985, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
ESULT 10
S-09-864-761-47985
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.6%; Score 37; DB 9; Length 15; 45.5%; Pred. No. 2.3; tive 4; Mismatches 2; Indels
                                                                                APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: BALDUR SVEINDA INSENDAL
APPLICANT: BALDUR SVEINDI INSENDAL
APPLICANT: BALDUR SVEINDI INSENDAL
TITLE OF INVENTION: BICACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT PELICATION NOWBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: REECED FOR WINDOWS VERSION 4.0
SEQ ID NO 8
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-788-869-8
; Sequence 8, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 45.5 Matches 5; Conservative
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RESULT 13 US-09-798-869-30

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Addrea E.
Applicant: Bekker, Linda-dail
APPLICANT: Bekker, Linda-dail
APPLICANT: The Government of the United States of America
APPLICANT: Department of the United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFERENCE: 015280-413100US
CURRENT APPLICATION NUMBER: US/09/88,320
CURRENT APPLICATION NUMBER: US 60/214,187
PRIOR APPLICATION UNBER: US 60/214,187
PRIOR FILING DAIE: 2000-06-26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 489
TYPE: PPT
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ORGANIZM: Mycobacterium tuberculosis
OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
3-09-888-320-2
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53.6%; Score 37; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 66;
Matches 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 9; Length 15; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                  PEDICALION NO. USAUGUSTATAL
APPLICANT: JOHN SIGNED SVENDERN
APPLICANT: JOHN SIGNED SVENDERN
APPLICANT: JOHN SIGNED SVENDERN
APPLICANT: BALDUR SVENDAÜGENSON
APPLICANT: BALDUR SVENDAÜGENSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,659
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSECEZ fOR WINDOWS VERSION 4.0
SEQ ID NO 30
LENTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESULT 15
S-09-738-626-5715
Sequence 5715, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
Sequence 30, Application US/09798869
Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.6%;
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: BOVINE
3-09-798-869-30
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Pred. No. 18;
5; Mismatches
                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JC 901 /38,626
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 5715
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 21, 2003, 08:11:57 Job time : 7.88372 secs
                                                                                                                                                        APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                    / TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-09-738-626-5715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.2%;
           IZOGUCHI, HIROSHI
IDO, SEIKO
                                               HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
NAKAGAWA, SATOSHI
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 FOWKRAMRKVR 12
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lactoferrin - goat
lactoferrin - shee
hypothetical prote
pyridoxamine 5'-ph
pyridoxamine 5'-ph
pyridoxamine 5'-ph
pyridoxamine 5'-ph
pyrodxerical prote
hypothetical prote
pyrotentical prote
dynein beta heavy
32K protein - vac
hypothetical prote
Alf. protein - vac
Alf. protein - vac
ADP, APP carrier pr
kinase-related pro
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
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probable vacuolar
hypothetical prote
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calnexin homolog -
                                                       February 21, 2003, 07:48:01; Search time 10.6047 Seconds (without alignments) . 108.784 Million cell updates/sec
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                                                                                                                                                                                          283224
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                          tal number of hits satisfying chosen parameters:
                                                                                                                                                                      283224 segs, 96134422 residues
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Maximum Match 100%
Listing first 45 summaries
                                     I protein - protein search, using sw model
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T28558
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A35774
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Gapop 10.0 , Gapext 0.5
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69
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Match Length DB
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rfect score:
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phytochrome - Scot	hypothetical prote	hypothetical prote	F1511.22 [imported	hypothetical prote	gene D5 protein -	33.3K hypothetical	transcription regu	gene 20 protein -	hypothetical prote	actin-like protein	calnexin - maize (	cytochrome P450 ho	cytochrome P450 CY	cytochrome P450 (C	cytochrome P450 CP
T09701	AC1714	AG1343	C96582	D82782	801975	G86403	G95232	WZBEM6	C33374	T41387	T03251	T04735	T07141	S62899	T07119
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30	31	32	33	34	3	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	ALIGNMENTS
	RESULT 1  TFHUL lactotransferrin precursor [validated] - human N.Alternate names: lactoferrin C.Species: Homo sapiens (man)
	C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #fext change Us-Dec-2000 C;Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S741 R:Cho. Y.
	submitted to the EMBL Data Library, March 1994 A.Reference number: G06820 A.Arceasion: G01304
	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
	A;KeBidues: 1-711 <chu> A;Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237 R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.</chu>
	Avitie: Complete nucleotide sequence of human mammary gland lactoferrin. A)Reference number: S11228; MUID:90384839; PMID:2402455 A.Accession: S11228
	A,Molecule type: mRNA A,Residues: 1.148', T.,150-422,'C',424-711 <rey> A,Cross-references: EMB:X53961; NID:g34415; PIDN:CAA37914.1; PID:g34416 R,Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.</rey>
<u> </u>	Mol. Endocrinol. b, 1987-1981, 1992 A,Title: Differential molecular mechanism of the estrogen action that regulates lactofer: A,Reference number: A45401; MUID:93125571; PMID:1480183 A,Accession: A45401 A,Molecule type: DNA
	A;Residues: 1-15 <ten> A;Residues: 1-15 <ten> A;Cross_references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312 A;Experimental source: placenta A;Note: sequence extracted from NCBI backbone (NCBIP:122202) R;Dowell: M.T.: Odden. J.E.</ten></ten>
	Nucleic Acids Res. 18, 4013, 1990 A; Title: Nuclectide sequence of human lactoferrin cDNA. A; Reference number: S10324; MUID:90326549; PMID:2374734 A; Accession: S10324 A; Accession: S10324
	A, Residues: 3-711 < POW> A, Residues: 3-711 < POW> A, Cross-references: EMBL:X52941; NID:934411; PIDN:CAA37116.1; PID:934412 A, Crowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W. Biochem. J. 276, 349-355, 1991 A, Title: Expression of cloned human lactoferrin in baby-hamster kidney cells. A, Reference number: S15853; MUID:91264786; PMID:2049066
	A,Accession: S1583 A,Status: nucleic acid sequence not shown, not compared with conceptual translation A,Molecule type: mENA A,Residues: 20-31 <sti> A,Accession: S20841 A,Molecule type: protein A,Residues: 20-28,'X',30-31 <st2></st2></sti>

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lactoferrin - sheep (fragment)
[Species: Ovis orientalis arises, Ovis ammon arises (domestic sheep)
[Species: Ovis orientalis arises, Ovis ammon arises (domestic sheep)
[Species: Ovis orientalis arises, Ovis ammon arises (domestic sheep)
[Spacies: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
[Spacies: 2.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
[Signia, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
[Signia, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
[Spacies: 1501ation and characterization of sheep lactoferrin, an inhibitor of platelet at A.Reference number: S52107; MUID:95127729; PMID:7827104
[A.Reference number: S52107]
[A.Reference number: S52107; MUID:95127729]
[A.Reference number: S52107; MUID:95127729]
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R,Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
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C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
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65.2%; Score 45; DB 2; Length 275;
Best Local Similarity 72.7%; Pred. No. 1.7;
Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                   Length 708,
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54.5%; Pred. No. 0.15;
tive 4; Mismatches
                                                                                                  DB 2;
                                                                                           Score 49; DB 2;
Pred. No. 0.79;
3; Mismatches
                                                                                                  71.0%;
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Best Local Similarity 63.6
Matches 7; Conservative
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Matches 6; Conservative
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U.Rado, T.A.; Wei, X.; Benz Jr., E.J.

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NIT. J. Biochem: lactotransferrin: amino acid sequence and structural comparisons with oth PARCEERIC number: A31000; MUID:85076667; PMID:6510420
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(Superfamily: transferrin; transferrin repeat homology)

(Superfamily: transferrin; transferrin iton binding; milk

(1-19/Domain: signal sequence #status predicted <81G>

(1-19/Domain: signal sequence #status experimental <MAT>

(1-19/Domain: signal sequence #status experimental <MAT>

(1-19/Domain: transferrin repeat homology <TRH1>

(1-10-36/Domain: transferrin repeat homology <TRH2>

(1-10-36/Domain: transferrin repeat homol
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V.Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4

V.Residues: 20-140,142-169,171-203,'L', 205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4

V.Residues: 20-140,142-169, Norskov, L.

Nur. J. Biochem. 241, 303-308, 1996

V.Fitler: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin (Febrence number: S74119) MUID:97054624, PMID:8898921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assignment of the relevant locus
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\(\text{Residues: 1-708 \infty} \)
\(\text{Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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lie Provost, F.; Nocart, M.; Guerin, G.; Martin, P.

Nocart, Commun. 203, 1324-1332, 1994

N.Title: Characterization of the goat lactoferin CDNA:

N.Reference number: JC2323; MJID:94380047; PMID:8093048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atus; not compared with conceptual translation
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Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ross-references: GDB:119368; OMIM:150210
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Gaps

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Length 208; Indels

Score 43; DB 2; Pred. No. 2.9; 1; Mismatches

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C;Superfamily: phytochrome, phytochrome homology Kskywords: chromoprotein, dimer; photocoreceptor; phytochromoprotein, dimer; photocoreceptor; phytochrome homology <PHX> F;65-581/Domain: phytochrome homology <PHX> F;321/Binding site: phytochromobilin (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Sorghum bicolor (sorghum)
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T14803
SACCESSION: T14803
Submitted to the BMBL Data Library, April 1996
A;Reference number: Z18186
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45.5%; Pred. No. 22;
ive 4; Mismatches 2; Indels
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A;Molecule type: mRNA
A;Residues: 1-1135 <CHI>A;Residues: 1-1135 <CHI>CGISCTOS: Teferences: EMBL:U56731; NID:g1800218; PID:g1800219
C;Genetics:
            A, Experimental source: strain 16M
C,Genetics:
A,Gene: BME115.1
A,Map position: I
C,Superfamily: pyridoxamine-phosphate oxidase
C,Keywords: oxidoreductase
                                                                                                                                                                                                                           62.3%;
ilarity 58.3%;
Conservative 1
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hes 5; Conservative
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Best Local Similarity
7; Conserv?
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A; Gene: CESP: F09C3.1
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Matches
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Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Harbere, 294, 2317-2323, 2001

Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         obable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - Brucella melitensis (Species: Brucella melitensis
Species: Brucella melitensis
Accession: 01-Feb-2002 #text_change 03-May-2002
Accession: AG341 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
DelVecorbio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Golteman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess oc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 P.H.; Hagius, S.; O'Callaghan, D.; Letess Title: The genome sequence of the facultative intracellular pathogen Brucella melitens Accession: AG341
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Date: il-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
1.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, itence 294, 2322-2328, 2001
Litle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     er, E.W.
Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
Reference number: AB2577; PMID:11743193
Accession: AB2670
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                                                                                                                                                     Status: preliminary
Molecule type: DNA
Residues: 1-206 <KUR>
Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:ġ15155733; GSPDB:GN00169
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Experimental source: strain C58 (Dupont)
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Molecule type: DNA
Residues: 1-208 «KUR»
Cross-references: GB:AE008917; PIDN:AAL52698.1; PID:g17983525; GSPDB:GN00190
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                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%; Score 43; DB 2; Length 206; 58.3%; Pred. No. 2.9; ive 1; Mismatches 4; Indels
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Pred. No. 2.9;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                    Gene: AGR C 1381
Map position: circular chromosome
Superfamily: pyridoxamine-phosphate oxidase
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Map position: circular chromosome
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Best Local Similarity 58.3%;
Matches 7; Conservative
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1es 7; Conservative
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Molecule type: DNA
Residues: 1-206 <KUR>
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A,Map position: 1
A,Introns: 53/2; 134/3; 283/1; 662/1; 731/3; 787/1; 976/3; 1043/2; 1171/3; 1267/2; 1354/?
                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 1-1391 < WIL>
A;Cross_references: EMBL:Z92781; PIDN:CAB07179.2; GSPDB:GN00019; CESP:F09C3.1
A;Experimental source: clone F09C3
hypothetical protein F09C3.1 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                  C; Accession: T20642
R; Lennard, N.
Rbuntted to the EMBL Data Library, March 1997
A; Reference number: 219304
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328 protein - vaccinia virus (strain WR) (fragment)
C;Species: vaccinia virus
C;Species: vaccinia virus
C;Species: vaccinia virus
C;Date: 25-dul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
C;Accession: A36415
R;Pacha, R.F.; Meis, R.J.; Condit, R.C.
A;Title: Structure and expression of the vaccinia virus gene which prevents virus-induces A;Reference number: A36415; MUID:90317884; PMID:2370683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: Z48758; NID: 9747879; PIDN: CAA88678.1; PID: 9747899; MIPS: YDR125c
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C;Species: Chlamydomonas reinhardtii
C;Species: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Accession: 108030
R;Mitchell, D.R.; Brown, K.S.
A; Call Sci. 107, 635-644, 199
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: 216302; MUID:94274778; PMID:8006077
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A;Map position: IX
B;Map position: IX

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N.Attriction protein YDR125c - yeast (Saccharomyces cerevisiae)
N.Attriction and s. Wypotherical protein YD9727.20c
C;Species: Saccharomyces cerevisials protein YD9727.20c
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
C;Accession: 55260
R;Murphy, L.; Shore, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Accession: 552600
A;Molecule type: DNA
A;Accession: 1453 «WUR>
A;Cossiques: 1453 «WUR>
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-456 <MIT>
A;Cross.reference: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
A;Experimental source: strain 21gr
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Best Local Similarity 41.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 3; Indels
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C; Keywords: nuclectide binding, P-loop
P,1919-1926/Region: nuclectide-binding motif A (P-loop)
F,2202-2209/Region: nucleotide-binding motif A (P-loop)
F,2530-2537/Region: nucleotide-binding motif A (P-loop)
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Janonymous, The C. elegans Sequencing Discovering Sequencing Discovering Sequencing Discovering Sequencing Sequencing Discovering Sequencing Discovering Sequencing Discovering Sequencing Discovering Sequencing Discovering Discovering
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;Alternate names: lactotransferrin
;Alternate names: lactotransferrin
;Paternate names: lactotransferrin
;Paterson: A28438; A41205
;Paterson: A28438; A41203
;Paterson: A28438; A412033; A41205
;Faterson: A28438; A412033; A41205
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Cross-references: GB:chr_1; PIDN:CAB07179.1; PID:g3875638; GSPDB:GN00019; CESP:F09C3.1
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.; Residues: 3-707 PENN>
.; Residues: BMBL: J03298
.; Liu, Y.; Teng, C.T.
.; Title: Chem. 266, 21880-21885, 1991
.; Title: Chem. 266, 21880-21885, 1991
.; Title: Chem. 266, 21880-21885, 1991
.; Reference number: A41205; MUID: 92042099; PMID: 1939212
                                                                                                                                                                                                                                                                                                           rotein F09C3.1 [imported] - Caenorhabditis elegans
Species: Caenorhabditis elegans
Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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V.Residues: 1-15 <LIU>
V.Cross-references: GB:N/74/78
V.Superfamily: transferrin; transferrin repeat homology
V.Superfamily: transferrin; transferrin predicted <SIG>
V.1-19/Domain: signal sequence #status predicted <SIG>
V.1-19/Domain: Lactorransferrin repeat homology TRH2>
V.358-695/Domain: transferrin repeat homology <TRH2>
V.494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 32;
2; Mismatches 3; Indels
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Pred. No. 40;
1; Mismatches
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59.4%; 70.0%;

Conservative

122 ÓWRRAMESVR 131

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Accession: A28438

3 QWKRAMRKVR

Query Match
Best Local Similarity
7; Conserv

Map position: 1 Gene: F09C3.1

Genetics:

Status: preliminary Molecule type: DNA

Ouery Match 58.0%; Best Local Similarity 54.5%; Matches 6; Conservative ;

CFOWKRAMRKV 11 37 CLRWONEMRKV 47

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ESULT 12

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Accession: A36415
Status: preliminary
Molecule type: DNA
Residues: 1-275 < PAC>
Cross-references: EMBL:M32064; NID:g335834; PIDN:AAA48348.2; PID:g7555635
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; 0 Ouery Match 55.1%; Score 38; DB 2; Length 275; Best Local Similarity 60.0%; Pred. No. 29; Matches 6; Conservative 1; Mismatches 3; Indels

1 CFOWKRAMRK 10

| :| || || 185 CLEWLRAKRK 194

Potherical protein Al7L - variola major virus
Species: variola major virus
Species: variola major virus
Species: variola major virus
Accession: T2858
Massung, R. F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Liur 366, 748-751, 1993
Title: Potential virulence determinants in terminal regions of variola smallpox virus
Reference number: Z20488; MUID:94088747; PMID:8264798
Accession: T2858
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-377 - AMA>
Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60868.1; PID:9439038
Experimental source: strain Bangladesh-1975

Gaps ö Query Match 55.1%; Score 38; DB 2; Length 377; Best Local Similarity 60.0%; Pred. No. 40; Matches 6; Conservative 1; Mismatches 3; Indels

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185 CLEWLRAKRK 194

arch completed: February 21, 2003, 08:02:48
b time : 12.6047 secs

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Submitted (MAY-1992) to
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TISSUE=Mammary gland;
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95.544 Million cell updates/sec
                                                                                                     February 21, 2003, 07:28:06 ; Search time 5.2093 Seconds
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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7LES_DROME SYB2_RHIME CCH1_CANAL NOV_CHICK GLGA_BACST NCAP_LYCVA NCAP_LYCVA NCAP_LYCVW ENV_HY2/CREPU PHY1_CREPU PHY1_CREPU PHY1_CREPU ATX1_ARATH TSGA_RAT
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hesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
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MEDLINE=90304639; PubMed=2402455;
Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                  21-JUL-1986 (Rel. 01, Created).
15-JUL-1999 (Rel. 38, Last sequence update)
La-JUL-1999 (Rel. 38, Last annotation update)
Lactorransferrin precursor (Lactoferrin) [Contains: Lactoferroxin Lactoferroxin B; Lactoferroxin C].
                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Mammary gland;
Liang Q., Jimenez-Plores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.",
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUTENCE FROM N.A.
TISSUE=Bone marrow;
Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region DNA
TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16786; Q16789; O00756; Q9H1Z3; Q96KZ4;
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TISSUE-Mammary gland;
TOSUE-Mammary gland;
TISSUE-Content M., Huan L.;
"CDNA Cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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TISSUE-Prostate;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[8]
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
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us-09-743-107b-93.rsp

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FEBS Lett. 142:107-110(1982).
                                                          SEQUENCE OF 436-711 FROM N.A.
                                                                     Blood 70:989-993 (1987).
                                                   lactotransferrin.",
SEQUENCE OF 20-711
                                                                                                                         resolution.
                                              Jolles P.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE-91166929; PubMed=1369293;
Tani F., Ilo K., Chima H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived"
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderer D.F.,
Hejtmanik J.F., Teng C.T., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T., T
                                                                                                                                                                                                                                             Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
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-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                 K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from human lactoferrin.";
Agric. Biol. Chem. 54:1803-1810(1990)
                                                                                                      Acta Crystallogr. D 55:403-407(1999).
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EMBL; U07643; AAB60324.1; -.
EMBL; M93150; AAA36159.1; -.
EMBL; M82302; AAA59511.1; -.
EMBL; M18642; AAA86665.1; -.
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CAA37116.1; -.
AAB57795.1; -.
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X52941; CAA37116.1;
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1LCT; 31-OCT-93.
1LFG; 31-JUL-94.
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21-APR-97.
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1LGB; 31-AUG-94
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MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norits G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J., Jolles P.;

"The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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Baker E.N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88001031; PubMed=3477300; Rado T.A., Well X., Benz E.J. Jr.; "Isolation of lactoferrin CDNA fr.; "Isolation of lactoferrin CDNA fr.; expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                                                                                                                                                                                MEDLINE=85076667; PubMed=6510420;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE=82046817; PubMed=6794640;
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                                                                                                                      Powell M.J., Ogden J.E., "Nucleotide sequence of human lactoferrin CDNA.";
Nucleic Acids Res. 18:4013-4013(1990).
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MEDLINE=97156796; PubMed=9003186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 670:243-254 (1981).
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MEDLINE=99190892; PubMed=10089347;
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                                                                                   MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 609-711.
MEDLINE=82262043; PubMed=7049727;
           OF 3-711 FROM N.A.
                                                   TISSUE=Mammary gland;
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77211 MW;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelus, Camelus.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Somali; TISSUB=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
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InterPro; IPR001156; Transferrin.
Pfam; PF00402; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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      Score 59; DB 1; Length 711;
Pred. No. 0.0028;
1; Mismatches 1; Indels
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LACTOTRANSFERRIN
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STANDARD; PR', Q9TUMO; Q9TUMO; Q9TUMO; Q9M2S5; 16-OCT-2001 (Rel. 40, Last sequents-JON-2002 (Rel. 41, Last annotted)
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       85.5%;
83.3%;
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                Local Similarity
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=94380047; PubMed=8093048;

MEDLINE=94380047; PubMed=8093048;

NEDLINE=94380047; PubMed=8093048;

NEDLINE=94380047; PubMed=8093048;

NEDLINE=94380047; PubMed=8093048;

NEDLINE=94380047; PubMed=8094 lactoferrin CDNA. Assignment of the relevant locus to bovine U12 synteny group.";

Biochem. Biophys. Res. Commun. 203:1324-1332(1994).

I- FUNCTION: TRANSFERAINS ARE LEON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.

I- SUBUNIT: NONOMER (BY SIMILARITY).

I- SUBCRELULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0B0C175A0B69D430 CRC64;
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SORBI
                                RESULT 4
PHYC SORBI
-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.

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                                                                                                                                                                                                       Interpro; Interpro; Italiansferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SNART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN_2; 2.
PROSITE; PS00206; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.

1 19 BX SIMILARITY.
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Pred. No. 0.19;
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Q -> K (IN REF. 2).
P -> P (IN REF. 2).
F -> P (IN REF. 2).
P -> P (IN REF. 2).
D -> G (IN REF. 2).
F2EDA3C83539960D CRC64;
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IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
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ANION (BY SIMILARITY).
ALINKED (GICNAC...)
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N-LINKED (GLCNAC.
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LACTOTRANSFERRIN
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Best Local Similarity 63.6%;
Matches 7; Conservative
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414
708 AA;
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                                                                                                                                                                                                                                                                                                                                                   CHILDER FROM N.A.

MEDLINE-97198556; PubMed=9046599;
CHILDER F.L., Miller J.E.,
Childe K.L., Miller J.E.,
Morgan P.W., Miller J.E.,
Morgan P.W., Miller J.E.,

"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phycochrome B.";

"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a cross service of the servic
                                                                                                                                                                  Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBUNIT: HOMODIMER (BY SIMILARITY).
-:- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-:- SIMILARITY: BELONGS TO THE PHYSCHROWE FAMILY.
-:- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-:- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
-:- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
PRT; 1135 AA
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InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004369; QAF.
InterPro; IPR004559; HIS XIN sig.
InterPro; IPR004661; His XiN sig.
InterPro; IPR001661; PAC.
InterPro; IPR001014; PAC.
InterPro; IPR001014; PAS. domain.
InterPro; IPR001294; Phytochrome.
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STANDARD;
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SMART; SM00388; HisKa;
SMART; SM00086; PAC; 1.
SMART; SM0091; PAS; 2.
                                                                                                                                          Phytochrome C.
                                                     16-OCT-2001 (
16-OCT-2001 (
15-JUN-2002 (
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Gaps

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1; Indels

3; Mismatches

|:||:| |||: 38 CYQWQRRMRKL 48 1 CFQWKRAMRKV 11

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us-09-743-107b-93.rsp

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HSSP, P02788; ICB6.
MGD; MG196837; Ltf.
InterPro; IPR001156; Transferrin.
PFINING; PR00422; TRANSFERRIN.
PRINING; PR00422; TRANSFERRIN.
PROSITE; P800205; TRANSFERRIN.
PROSITE; P800205; TRANSFERRIN.
PROSITE; P800207; TRANSFERRIN.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.0%; Score 40; DB 1; Length 707; 54.5%; Pred. No. 8.8; 3; Indels ive 2; Mismatches 3; Indels
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-> V (IN REF. 1).
F26AE0340A4C19A8 CRC64;
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IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
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LACTOTRANSFERRIN
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PHYC_ORYSA STANDARD; PRT; 1137 AA.

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

PHYC.
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     EMBL; BC006904; AAH06904.1;
EMBL; M74778; AAA39427.1; -.
PIR; A28438; A28438.
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Matches 6; Conserv
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PHYC ORYSA
LD PHYC OLYCO
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DT 16-OCT
DT 15-OCT
DD PHYCOI
GN PHYCOI
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MIDLINE=92042099; PubMed=1939212;

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

J. Biol. Chem. 266:21880-21885(1951).

-! FONGTION: TRANSFERRING ARE IRON BINDING TRANSPORT PROTEINS WHICH
-LANGTION: TRANSFERRING ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-! SUBCELLULAR LOCATION: Secreted.
-! SUBCELLULAR LOCATION: Secreted.
-! DOWAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-! SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
PROSITE; PS00245; PHYTOCHROME_1; FALSE_NEG.
PROSITE; PS50046; PHYTOCHROME_2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Repeat; Mulligarian; Photoreceptor; Phytochrome; Chromophore; DOMAIN 618 688 1.
DOMAIN 748 822 PAS 1.
DOMAIN 902 HISTIDINE KINASE.
BINDING 321 321 CHROMOPHORE (BY SIMILARITY).
SEQUENCE 1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87280033; PubMed-3611056;
Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                    DB 1; Length 1135;
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TISSUBELLerus;
Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P08071; P70690; Q61799; Q922P2; U1-AUC-1988 (Rel. 08, Created) 15-UN-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                    Score 42; DB :
Pred. No. 6.2;
4; Mismatches
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J. Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                    60.9%;
45.5%;
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                                                                                                                                                                                                                                                                                                                      5; Conservative
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775 CLEWNKAMQKI 785
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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
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FL_MOUSE
TRFL_MOUSE
P08071; P70
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·,

Oryza sativa (Rice). Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae; Ehrhartoideae, Oryzeae, Oryza.

NCBI\_TaxID=4530;

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IN MOI. BEGIL BYOL. 13:1141-1150 (1996).

IN MOI. BEGIL BYOL. 13:1141-1150 (1996).

IN MOI. BEGIL BYOL. 13:1141-1150 (1996).

IN THE REGULATORY PHOTORECEPPOR WHICH EXISTS IN TWO FORMS THAT ABSORBS MAXIMALLY IN THE FAR-RED BY ENGING THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONFESSION OF PR IN PERSONS RECONVERSION OF PR IN PRESENCE AND ARRAY OF WORPHOGENIC RESPONSES, WHEREAS RESPONSES, PER CONTROLS THE EXPENSION OF A NUMBER OF NICLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPROSPHYTE CARBOXYTLASE, CHHOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDICTASE, RRWA, ETC. IT ALSO CONTROLS.

IN SHAPPENSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.

IS SHAPPENSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.

IS SHALLARITY: BELONGS TO THE PHYTOCHROME FAMILY.

IS SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

IS SIMILARITY: CONTAINS OR EXAMINATED THE SAMILY.

IS SIMILARITY: CONTAINS 1 PASS-ASSOCIATED C-TERMINAL (FAC) DOWAIN.
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R Pfam; PF02518; HATPase c; 1.

R PRINT; SW00065; GAF; 1.

R SMART; SW00065; GAF; 1.

R SMART; SW00091; HATPase c; 1.

R SMART; SW00096; PAC; 1.

R SMART; SW00091; PAS; 2.

R R SMART; SW00091; PAS; 2.

R R SMART; SW00091; PAS; 2.

R R SMART; SW00094; PAS; 1.

R R SMART; SW00094; PAC; 1.

R R SWART; SW00094; PATTOCHROME 1; 1.

R PROSITE; PS50046; PHYTOCHROME 1; 1.

R PROSITE; PS50046; PHYTOCHROME 2; 1.

R REPROSITE; PS50046; PHYTOCHROME 2; 1.

R REPROSITE; PS50046; PHYTOCHROME 2; 1.

R REPROSITE; PS50046; PHYTOCHROME 2; 1.
SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare,
Tahir M., Kanegae H., Takano M.;
"Phytochrome C (PHYC) gene in rice: isolation and characterization of
a complete coding sequence.";
(In) Plant Gene Register PGR98-210.
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 275-378 FROM N.A. MEDILINE=97019052; PubMed=886568; MATHEWS S., Sharrock R.A.; "The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR003594; Arpbind Arpase.
Interpro; IPR003169; GAF.
Interpro; IPR001661; His_KIN sig.
Interpro; IPR001661; His_Kin Sig.
Interpro; IPR001601; PAC.
Interpro; IPR001014; PAC.
Interpro; IPR00114; PAC.
Interpro; IPR001294; Phytochrome.
Fram; PF00360; phytochrome; 1.
Fram; PF00360; phytochrome; 1.
Fram; PF0036012; signal; 1.
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EMBL; U61207; AAB41996.1; -.
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SEQUENCE FROM N.A.

SEQUENCE STAINBEACKELEY, HOLF R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gazle R.F., Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gazle R.F., Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., Sutron G.G., Wortman J.E., Yandell M.D., Zhang O., Chen L.K., Bratch G.G., Mortman J.E., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Man K.H., Doyle C., Baxendell W.D., Payraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Berman B.P., Brandari D., Bolankov S., Ballew R.M., Basu A., Berman B.P., Brandari D., Bolankov S., Borkova D., Botchan M.R., Bouck J., Broketein P., Botchier P., Botchan M.R., Bouck J., Broketein P., Botchar I., Botke C., Davenport L.B., Davies P., Datz S.M., Borkova D., Delcher A., Dang Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dokson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dokson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Barris M., Garriellan A.E., Garra C., Ferraz C., Ferra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapox Insecta, Petrygota, Nooptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
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0
                                                                                                                                                        Score 40, DB 1; Length 1137;
Pred. No. 15;
3; Mismatches 3; Indels
                                       HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY)
                                                                                                                     125982 MW; F2A520181CFE7B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                          F -> S (IN REF. 2)
C -> S (IN REF. 2)
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30-74X7-2000 (Rel. 39, Created)
30-74X7-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             292 AA
PAS 1.
PAS 2.
                                                                                                                                                             58.0%;
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620 690
750 82,
904 112,
322 32;
279 27,
292 292
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Best Local Similarity
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NLA OR CG6072.
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Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.;
J. Cell Sci. 107:635-644(1994).
-!- FUNCATION: PORCE GENERALING PROTEIN OF BUXARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBLES DYNEIN HAS ATPASE ACTIVITY.
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.(Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C.; "The genome sequence of Drosophila melanogaster."; science 287:2185-2195(2000).
-I- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALPHA, BETA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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InterPro; IPR004273; Dynein_heavy.
Pfam; PP03028; Dynein_heavy; 1.
Colled coil.
Colled coil.
277 293 COLLED COIL (POTENTIAL).
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-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0026629; nla.
SEQUENCE 292 AA; 31423 MW; 64FlBBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.5%; Score 39; DB 1;
54.5%; Pred. No. 5.3;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-NAV-2000 (Rel. 39, Last annotation updat
Dynein beta chain, flagellar outer arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94274778; PubMed=8006077;
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Matches 6; Conserv
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SEQUENCE FROM N.A.
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Q39565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Planet P., Jagoueix S., Bove J.M., Garnier M.; "Jagoueix Screening "Detection and characterization of the African Citrus Greening Liberobacter by amplification, cloning and sequencing of the rplKAJi.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
11-NOV-21001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBDIVIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND BETA' CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
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COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
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ATP (POTENTIAL).
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InterPro; IPR001572; RNA_pol_B.
PEOSITE; PS01166; RNA_Pol_B; 1.
PROSITE; PS01166; RNA_Pol_BETA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
NON TER
SEQUENCE 146 AA; 16731 MM; 815D6EDD66FDA943 CPCCA.
                                                                                                                                                                                                      9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                56.5%; Score 39; DB 41.7%; Pred. No. 96; tive 4; Mismatches
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519961 MW;
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2530 253
2879 288
4568 AA;
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Jirology 179:247-266(1990)
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                           COMPLETE GENOME
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TLCE_RICPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Al6L.
Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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MEDINE=91021027; PubMed=2219722;
Geobel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.,
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               Indels
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                 4.
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                                                                                                                                                                         01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein Al6 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
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  Pred. No. 3.9;
0; Mismatches
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60.08;
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NON TER 275 275
SEQUENCE 275 AA: 1111
  Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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NCBI_TaxID=10249;
                                                                                                                                                                                                                                                          Orthopoxvirus.
NCBI_TaxID=10254;
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01-FEB-1991 (
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P16710;
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A16_VACCC
D _VA16_VAC
C P20993;
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MEDLINE=97419517; bubmed=9274032;
MEDLINE=97419517; bubmed=9274032;
Medenanic rearrangements during evolution of the obligate
intracellular parasite Rickettsia prowazekii as inferred from an
analysis of 52015 bp nucleotide sequence.";
Microbiology 143:2783-2795(1997)
-:- FUNCTION: PROVIDES THR RICKETTSIAL CELL WITH HOST ATP IN
EXCHANOE FOR RICKETTSIAL ADP. THIS IS AN OBLIGATE EXCHANGE SYSTEM.
THIS ENERGY ACQUIRING ACTIVITY IS AN IMPORTANT COMPONENT OF
RICKETTSIAL PARASITISM (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- SIMILARITY: BELONGS TO THE ADP/ATP TRANSLOCASE TLC FAMILY.
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Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.,
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0
                                                                      "Appendix to 'The complete DNA sequence of vaccinia virus'.";
Virology 179:517-563(1990).
-!- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.
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16-00T-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein 5 (ADP/ATP translocase 5).
TLCE OR TLCS OR RP739.
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NCBI_TaxID=782,
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MEDLINE=99039499; PubMed=9823893;
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INTERFOY, IPRO04667; ADP_ATP_car.
Pfam, PF03219; TLC; 1.
TIGRPAMS; TIGR00769; AAA; 1.
TIGRPAMS; TIGR00769; AAA; 1.
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Gaps ; Length 500; 3; Indels Score 38; DB 1; Pred. No. 14; 2; Mismatches 55.1%; 6; Conservative Query Match Best Local Similarity Matches 6; Conser

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01-NOV.1998 (Rel. 09, Created) 01-NOV-1998 (Rel. 09, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Envelope polyprotein (GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]. 856 AA PRT; STANDARD; ENV HV2NZ P05883;

(isolate NIH-Z) (HIV-2) Human immunodeficiency virus type 2 (isolate NIH-Z) Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI\_TaxID=11719;

SEQUENCE FROM N.A.
MEDLINE=88320359; PubMed=3261862;
Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R., Hall L., Fargnoli K., Jagodzinski, L.L., Guo H.-G., Laure F.,
Arya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.,
"Genetic variability between isolates of human immunodeficiency virus

(HIV) type 2 is comparable to the variability among HIV type 1."; Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).

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EMBL; J03654; AAB00761.1; -

InterPro; IPR000328; Env GP41. InterPro; IPR00777; GP120. Pfam: PF005116; GP120, 1. Pfam; PF00517; GP41; 1. AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;

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Drosophila virilis (Fruit fly). Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila. NCBI\_TaxID=7244; 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Sevenless protein (EC 2.7.1.112). PRT; 2594 AA. STANDARD; 7LES DROVI P20806; 7LES\_ 

Drosophila melanogaster.";
Proc. Natl. Acad. Sci. U.S.A. 87:5351-5353(1990).
-!- FUNCTION: RECEPTOR FOR AN EXTRACELLULAR SIGNAL REQUIRED TO
INSTRUCT A CELL TO DIFFERENTIATE INTO A R7 PHOTORECEPTOR. THE
LIGAND FOR SEV IS THE BOSS (BRIDE OF SEVENLESS) PROTEIN.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein MEDLINE=90319110; PubMed=2115169; Michael W.M., Bowtell D.D.L., Rubin G.M.; "Comparison of the sevenless genes of Drosophila virilis and SEQUENCE FROM N.A.

tyrosine phosphate. RECEPTOR SUBFAMILY

SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS. CAUTION: UNCLEAR WHETHER THE POTENTIAL MEMBRANE SPANNING REGION NEAR THE N-TERMINUS IS PRESENT AS A TRANSMEMBRANE DOMAIN IN THE 

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                                                                                                                                                                                                                                                                                                      EMBL; M34545, AAA28883.1; -...

R EMBL; M34544, AAA28883.1; JOINED.

R PIR, A35774, A35774.

R HSSP; P11362; IFCK.

R HSSP; P11362; IFCK.

R InterPro; IPR000119; Euk pkinase.

R InterPro; IPR000391; Euk pkinase.

R InterPro; IPR00123; LdI receptor rep.

R InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R Pfam; PP000604; fm3; 6.

R Pfam; PR000604; fm3; 6.

R SWART; SW00107; PROFIEIN KINASE ATP; 1.

R SWART; SW00109; PROFIEIN KINASE ATP; 1.

R PROSITE; PS00109; PROFIEIN KINASE TYR; 1.

R PROSITE; PS00109; PROFIEIN KINASE DOM; 1.

R PROSITE; PS00109; PROFIEIN KINASE TYR; 1.

R PROSITE; PS00109; PROFIEIN KINASE TYR; 1.

R PROSITE; PS00109; PROFIEIN KINASE DOM; 1.

R PROSITE; PS00109; PROFIEIN KINASE TYR; 1.
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FIBRONECTIN TYPE-III 2.
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FIBRONECTIN TYPE-III 6.
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                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Rukaryota; Viritdiplantae; Streptophyta; Eubryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R EMBL; U08315; AAA17742.1; -...

R InterPro; IPR001580; Calreticulin.

R PERMIN; PR00626; Calreticulin; 1.

R PROSITE; PR00686; CALRETICULIN 1; 1.

R PROSITE; PS00809; CALRETICULIN 2; 1.

R PROSITE; PS00809; CALRETICULIN Z; 1.

R ROSITE; PS00806; CALRETICULIN REPEAT; 3.

W Calcium-binding; Endoplasmic reticulum; Transmembrane; Signal; CALRIN 26 528 CALNEXINAL.

T SINAL; Chaperrone.

T GAINAL; Chaperrone.

T CHAIN 26 528 LOWENTIAL.

T TRANSMEM 467 487 POTENTIAL.

T DOMAIN 277 233 4 A APPROXIMATE REPEATS.

T REPEAT 264 255 1-2.

T REPEAT 263 274 1-3.

T REPEAT 263 274 1-3.
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Score 38; DB 1; Length 2594; Pred. No. 81; 2; Indels 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CV. COlumbia;
BOYCe J., Coates D., Evans D.;
"Genomic sequence of a calnexin homologue from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPROXIMATE REPEATS
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 Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative '
                                                                               305 CAĆWYRALKEI 315
                                                     1 CFQWKRAMRKV 11
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REPEAT
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SEQUENCE 528 AA; 60017 MW; C888DA1391B651EE CRC64;

0; Gaps Query Match Best Local Similarity 50.0%; Pred. No. 23; Matches 5; Conservative 3; Mismatches 2; Indels

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1 CFQWKRAMRK 10 | :||| |:: 315 CGEWKRPMKR 324

arch completed: February 21, 2003, 07:51:40 b time : 6.2093 secs

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Q8vwml triticum ae Q6fs16 homo saplen P88213 human immun Q68841 horseradish Q8xse2 ralstonia s Q9u054 giardia lam Q04623 accharonyc Q8unfs human immun Q77855 human immun Q77855 human immun Q7823 human immun Q98ml2 cicer ariet Q8sml2 cicer ariet Q8sml2 cicer ariet Q85389 variola may Q8122 vaccinia avi Q8122 vaccinia avi Q8v2n9 camelpox viru Q9mls homo saplen Q9xfx1 cicer ariet Q8v2n9 camelpox viru Q9mls homo saplen Q9xfx1 cicer ariet Q8v2n9 camelpox viru Q9mls homo saplen Q9xfx1 cicer ariet Q9xfx1 cicer ariet Q8v2n9 camelpox viru Q9mls homo saplen Q9xfx1 cicer ariet Q9xfx1 cice
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Lactotransferrin.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Primates; Catarrhini, Hominidae; Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC2247; AAH2347.1; -
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 AA
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Q9M7A9
Q9GNW1
Q9GNW1
Q9E8H5
Q6B5213
Q6B5213
Q9C054
Q0C054
Q0C054
Q0C0623
Q9C0623
Q9CM12
Q9SML1
Q9SML
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TISSUE=PROSTATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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  Q9UCY5
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Q9ucy5 homo sapien
Q9ucy5 homo sapien
G9r80 ovis aries
Q93780 caenorhabdi
Q86a0 rhizobium 1
Q8uhc2 arrobacteri
Q8rk3 brucella me
Q8yk8 lycopersico
Q1418 human immun
Q1772 caenorhabdi
Q9x65 human immun
Q9x675 human ind
Q9x671 sesamum ind
Q9x671 homo sapien
Q95m21 homo sapien
                                                                                                                                                                                   2003, 07:44:43 ; Search time 21.6744 Seconds (without alignments) 114.078 Million cell updates/sec
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                          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
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Q9UCY5
Q9UCY5
Q91780
Q98780
Q92RH8
Q92RH8
Q92RH8
Q1771
Q17772
Q9XFD5
Q9XFD5
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Gapop 10.0 , Gapext 0.5
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sp archea.*
sp bacteria.*
sp fungi.*
sp invertebrate.*
sp mammal.*
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sp_rvirus:*
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Match Length DB
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MEDLINE=99069613; PubMed=9851916;
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les 7; Conservative
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262 FQWKISMRKTR 272
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DNA Res. 7:331-338
  SEQUENCE FROM N.A.
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Q986A0;
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QBUHCZ
AC QBUHCA
DD 01-JD
DT 01-JD
DE PYTIC
GN PDXH
GN PDXH
OS AGTO
OC RHIZE
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  SORFFRE
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F53H4.4 protein.
F53H4.4. Metacas, Reagans.
Caenorhabditis elegans.
Bukaryota; Metacas, Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                             SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
Sato I.;
Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9TR80;
01-MAY-2000 (TERMELE1. 13, Created)
01-MAY-2000 (TERMELE1. 13, Last sequence update)
01-UMY-2001 (TERMELE1. 17, Last annotation update)
00-UMA-2001 (TERMELE1. 17, Last annotation update)
Lactoferrin (Fragment).
00-UMB aries (Sheep).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Cetartiodactyla; Ruminantia; Pecora, Bovoidea,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                          Length 38;
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Pred. No. 0.26;
4; Mismatches 1; Indels
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Dobson R.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
[2]
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MEDLINE=55127729; PubMed=7827104;

MEDLINE=55127729; PubMed=7827104;

Bidan Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;

Biochim. Biophys. Acta 1243:25-32 (1995).

HSSP; O77698; ICE2.

HINCEPPO; IPRO01156, Transferrin.

Pfam, PG00405; transferrin; 1.

SEQUENCE 33 AA; 3914 MW; D1904CAR15A73961 CRC64;
                                                                                                                                                                                           seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 18XA.
HTCPPCO, IPRO01156, Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402P490B5EBDDEB CRC64;
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81.8%; Pred. No. 0.058;
iive 1; Mismatches
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54.5%;
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Best Local Similarity 54.2
Las 6; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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19 CYQWQXKMRKL 29
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                                                                                                                                                                                                                                                     Gaps
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01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
Pyridoxamine 5'-phosphate oxidase.
PDXH OK ATUOTGO OR AGR C. 1381.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision, Rhizobiaceae group;
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"Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                    Length 275;
                                  investigating biology.";
Science 282:2012-2018 [19.9].
EMBL; Z81099; CAB03137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
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Last annotation update)
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Local Similarity 72.7%; Pred. No. 3.2;
les 8; Conservative 1; Mismatches ;
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TIGRPAMs; TIGR00558; pdxH; 1.
PROSTIE; PS01064; PYRIDOX OXIDASE; 1.
CEMPLETE Proteome
SEQUENCE 205 AA; 23300 WW; OBADRA!
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InterPro; IPR000659; Pyridox oxidase.
Pfam; PF01243; Pyridox_oxidase; 1.
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Gaps

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us-09-743-107b-93.rspt

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SEQUENCE FROM N.A.
SETRALIA-IGM / ATCC 23456 / BIOTYPE 1;
MEDLINE-END / ATCC 23456 / BIOTYPE 1;
MEDLINE-END / ATCC 23456 / BIOTYPE 1;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
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Lycopersicon esculentum (Tomato).

Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;

Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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Brucellaceae, Brucella.
NCBL_TaxID=29459;
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                                                                                                                                                                                                                                  Length 206
                                                                                                                                                                                                                                                                                                                     4; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MD-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5).
BMEII517.
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TIGRFAME; TIGRO0558; pdxH; 1.
PROSITE; PS01064; PYRIDOX OXIDASE; UNKNOWN_1.
Oxidoreductase; Complete Proteome.
SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
EMBL; AB09587; AAL52698.1; ---
InterPro; IPR00559; Pyridox_oxidase.
Pfam; PF01243; Pyridox_oxidase; 1.
ProDom; PD006312; Pyridox_oxidase; 1.
ProDom; PT0GRPAMs; TIGR00558; pdxH; 1.
PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
Oxidoreductase; Complete protesome.
SEQUENCE 208 AA; 23866 MW; CBIF50BC9612DE28 CRC64;
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Last annotation update)
                                                                                                                                                                                                                        62.3%; Score 43; DB 16; 58.3%; Pred. No. 5.5;
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Pred. No. 5.5;
1; Mismatches 4,
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Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                           Best Local Similarity 58.3
Matches 7; Conservative
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MEDIJNB=21608531; PubMed=11743194;

Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

Goodner B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

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Agrobacterium tumefaciens CS8.",

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EMBL; AE008043; AAL41776.1; -
                                                                                                                   MEDLINE-21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Exymond C., Rouse G., Saemphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome of the natural genetic engineer Agrobacterium tumefaciens CS8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrENBLrel. 19, Created)
01-DEC-2001 (TrENBLrel. 19, Last amoctation update)
01-DEC-2002 (TrENBLrel. 21, Last amoctation update)
01-JUN-2002 (TrENBLrel. 21, Last amoctation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
(EC 1.4.3.5)
PDXH OR R00895 OR SMC00069;
Rhizobium mellioti (Sinorhizobium mellioti).
Rhizobiaceae; Sinorhizobium.
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Belstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Irlaure V., Masuy D.,
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EMBL: ALSS1785; CAC45467.1,
InterPro; IPR000659; Pyridox oxidase.
Pfan; PF01243; Pyridox_oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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[1]
[2]UCBUCE PROM N.A.
STRAIN=1021;
MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nery Match 62.3
Sest Local Similarity 58.3
fatches 7; Conservative
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         NCBI_TaxID=176299;
                                                                                            SEQUENCE FROM N.A.
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Q92RH8

88

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Gaps

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Gaps

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Indels

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Mismatches Pred. No.

7

70.0%;

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7; Conservative
Best Local Similarity
Matches 7; Conserv
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Q9XFD5;
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                                                                                                                                                RESULT 11
017772
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MEDLINE=94187055; PubMed=8139000;
Grez M., Detrich U., Balfe P., Von Briesen H., Maniar J.K.,
Mahambre G., Delwart B.L., Mullins J.I., Ruebeamen-Waigmann H.;
"Genetic analysis of Human immunodeficiency virus type 1 and 2 (HIV-1 and HIV-2) mixed infections in India reveals a recent spread of HIV-1 and HIV-2 from a single ancestor for each of these viruses.";
EMBL; U07108; AAA17669.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                      "Characterization of the gene encoding the apoprotein of phytochrome B2 in tomato, and identification of molecular lesions in two mutant alleles.";
               Kerckhoffs L.H., Kelmenson P.M., Schreuder M.E., Kendrick C.I.,
Kendrick R.E., Hanhart C.J., Koornneef M., Pratt L.H.,
Cordonnier-Pratt M.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGR00229; Bensory box; 2.
PROSITE; PS00061; ADH SHORT; UNRNOWN 1.
PROSITE; PS00245; PHYTOCHROME 1. 1.
PROSITE; PS0046; PHYTOCHROME 2; 1.
SEQUENCE 1121 AA; 125308 MM; ED9EDA704BB37F27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58165 MW; 9B103784A08DCB9C CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 2.
Viruses, Retroid viruses, Retroviridae; Lentivirus.
NCBI_TaxID=11709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 AA
                                                                                                                                           EMBL, AF122901, AADS0631.1;
InterPro; IRR02198; ABH ehort.
InterPro; IRR03198; ABH ehort.
InterPro; IRR03018; GAF.
InterPro; IRR03601; His kinA.
InterPro; IRR03601; His kinA.
InterPro; IRR001610; PAC.
InterPro; IRR001010; PAC.
InterPro; IRR001014; PAS. Commain.
InterPro; IRR001014; PAS. Commain.
InterPro; IRR001014; PAY. Commain.
InterPro; IRR001014; Phytochrome.
                                                                                                                           Mol. Gen. Genet. 261:901-907(1999).
EMBL; AF122901; AAD50631.1; -.
MEDLINE=99413290; PubMed=10485280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
NON_TER 508 508
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Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase c; 1.
                                                                                                                                                                                                                                                                                                                                 PF02518; HATPase_c; 1.
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWART; SM00388; Hiska; I.
SWART; SM00086; PAC; I.
SWART; SM00091; PAS; 2.
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Best Local Similarity 54.5
Matches 6; Conservative
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ENV.
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SEQUENCE
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Q74118;
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Score 41; DB 15; Length 508;

59.48;

Query Match

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                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome P450 (Fragment).
Oryza sativa (Rice).
Oryza sativa (Rice).
Streptophyta; Enreptophyta; Embryophyta; Tracheophyta;
Enrartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu J., Yang J., "Suppression subtractive hybridization (SSH) identified candidate genes that are differentially expressed at rice young panicle.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018[198].
BMBL: Z92781; CABO7179.2;
InterPro; IPR000148; IQ region.
InterPro; IPR0001936; RasGAP.
InterPro; IPR0001936; RasGAP.
InterPro; IPR0001936; RasGAP.
InterPro; IPR0001936; RasGAP.
InterPro; IPR0001936; RasGAP.C.
Pfam; PF00612; IQ; 1.
ProDom; PD008135; RasGAP.C; 1.
SMART; SM00013; IQ; 1.
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PROSITE; PS50018; RAS GIPASE ACTIV 2; 1.
SEQUENCE 1391 AA; 159210 MW; 794DF9EBFA2E65AC CRC64;
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submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Pred. No. 83;
1; Mismatches
                                                                                                                                             PRT; 1391 AA.
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                F09C3.1.
Caenorhabditis elegans.
                          340 KWKEAMREVR 349
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3 OWKRAMRKVR 12
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Best Local Similarity
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2S albumin
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Q96M21
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Van der Loeff, Whittle H., Breuer J.;
Mortality among human immunodeficiency virus type 2-positive
J. Virol. 72:7895-7899(1998).

BMBL, AURILES, CAAOSSBO.1;

InterPro, 11PRO0077, GP120.

Pfam; PP00516; GP120; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A, MEDLINE=97255645; PubMed=9100992; MEDLINE=97255645; PubMed=9100992; Xiang Z., Ariyoshi K., Wilkins A., Dias F., Whittle H., Breuer J.; "HIV type 2 pathogenicity is not related to subtype in rural guinea bissau.";
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0
                                                                                                                                                                  58.0%; Score 40; DB 10; Length 105;
60.0%; Pred. No. 9.6;
ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.0%; Score 40; DB 15; Length 126; 60.0%; Pred. No. 12; ive 4; Mismatches 0; Indels
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AF140486; AAD29699.1; -.
InterProf. IPR001128; Cytochrome_P450.
                                                                                                                                   SEQUENCE 105 AA; 11912 MW; BOEEFCDD487E19F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 AA; 14891 MW; 24882B768F66F88B CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBL_TaxID=11709;
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AIDS Res. Hum. Retroviruses 13:501-505(1997).
                                                             Pfam; PF00067; p450; l.
PRINTS; PR00385; P450.
PROSITE; P500086; CYTOCHROME P450; UNKNOWN l.
Heme; Monooxygenase; Oxidoreductase.
NON TER
                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coat protein; Glycoprotein.
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CQ9XHP1;
01-NOV-1999 (TFEMBLrel. 12,
01-NOV-1999 (TFEMBLrel. 12,
01-MAR-2002 (TFEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                               Envelope protein (Fragment)
                                                                                                                                                                                Local Similarity 60.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                            61 CPOWERLGKK 70
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72 EWKRAMQEVK 81
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XHP1
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EMBL, AR054453; Bab71493.1; Submit Seguence 274 AA; 30083 MW; IDD43654D4135B2F CRC64;
                                                                                                                                                                                                                                                                         Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C., "Molecular cloning of 11S globulin and 2S albumin, the two major seed
Sesamum indicum (Oriental sesame) (Gingelly).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Lamiales, Pedaliaceae, Sesamum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q96M21;

Q1-DEC-2001 (TEMBLrel. 19, Created)

O1-DEC-2001 (TEMBLrel. 19, Last sequence update)

O1-DEC-2001 (TEMBLrel. 19, Last annotation update)

CDNA FLJ32891 fis, clone TEST12004929.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                             storage proteins in sesame.";
J. Adric. Food Chem. 4714932-4938(1999).
EMBL, AF091841, AAA1-2943.1;
InterPro; IPR000617; Majin.
InterPro; IPR000617; Majin.
InterPro; IPR00168; Try/amyl inhbtr.
Pfam; PF00234; tryp alpha amyl; 1.
PRINTS; PR00499; AAI; 1.
SEQUENCE M0499; AAI; 1.
SEQUENCE M0499; AAI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                MEDLINE=20074970; PubMed=10606554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.0%;
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Query Match
Best Local Similarity 66,77,
Best Local Similarity 66,77,
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                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=TAINAN 1;
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TISSUE=TESTIS;
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RESULT 1
AAY78094
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1:=/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Human lactoferrin	n lactoferrin n lactoferrin
escr	Huma Huma Huma Huma Huma Huma Huma	Huma
SUMMARIES	AAY78094 AAY78070 AAY78091 AAX78092 AAY78038 AAY78046 AAY78084	AAY 78037 AAY 78048
DB	, , , , , , , , , , , , , , , , , , ,	
% Query Match Length DB		13
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Result No.	H 01 W 4 10 10 7 18 18	н 0

Dolphin GT;

Baltzer L,

Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13

Human lactoferrin Human lactoferrin Human lactoferrin	Human lactoferrin Peptide for anti-u Human lactoferrin	lactof	-	Human lactoferrin		Human lactoferrin	_		Advanced glycosyla	Human lactoferrin	Amino acid sequenc	n lacto		-rel	Lactoferrin derive		errin	a)		Bovine lactoferrin	Anti-parasitic lac	Anti-parasitic lac	Peptide for anti-u	rin	Lactoferrin-derive	. Lactoferrin derive	Lactoferrin-derive	Lactoferrin-derive
21 AAY78049 21 AAY78036 21 AAY78050	21 AAY78051 17 AAR98554 21 AAY78035	1 AAY7806		21 AAY78064 21 AAY78065	AAY7803		AAY7806		AAW1339	21 AAY78033	21 AAY68867		m	4 AAR448	15 AAR48530			ıvı ·	16 AAR84698	16 AAR84699	6 AAR8026	16 AAR80264	AAR985		17 AAW03045	17 AAR90607	AAR8762	17 AAR87622
Ц Ц Ц В <b>4.4</b> .	11. 15. 7.	1 L L	91	91.0	11	17	17	18	18	18	13	13	50	20	50	20	20	20	20	20	20	20	20	20	20	20	20	20
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## ALIGNMENTS

Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative. Human lactoferrin derived peptide SEQ ID NO:94. AAY78094 standard; Peptide; 12 AA 98SE-0002441. 98SE-0002562. 98SE-0004614. 99WO-SE01230. (first entry) (ASCI-) A+ SCI INVEST AB. WO200001730-A1. 06-JUL-1998; 17-JUL-1998; 29-DEC-1998; Homo sapiens. Synthetic. 25-APR-2000 06-JUL-1999; 13-JAN-2000. AAY78094; 

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the circoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and Candida infection on a mucosal curinary tract infections and/or tumours. The peptides can also be used sufficed and pacterical and pacterical and macterial and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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100.0%; Score 70; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 12; Conservative 0; Mismatches 0: Tndele
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98SE-0004614.
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Synthetic.
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17-JUL-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human

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Gaps ; 0

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as usinary tract infections, collitis, and Candida infections on a mucosal membrane) inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used fungicidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 0.00014;
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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17-JUL-1998;
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Gaps

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferzin. The peptides are taken up in the intestine through binding to specific lactoferzin receptors and are the ntransported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Been though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
             Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.
fungicidal and bactericidal and may also be used as preservatives
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                                                                                                                                                                              Score 65, DB 21; Length 12;
Pred. No. 0.0002;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                     AAY78092 standard; Peptide; 12 AA.
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                                                                                                                                                                              92.98;
91.78;
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98SE-0004614.
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Best Local Similarity 91.7
Matches 11, Conservative
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29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food atuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Been though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would contain them to be used for the same purposes as lactoferrin at lower
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83.3%; Pred. No. 0.00095;
tive 1; Mismatches 1; Indels
                                         92.9%; Score 65; DB 21; Length 12; 91.7%; Pred. No. 0.0002; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                     AAY78038 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
                                             Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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Matches 10; Conserval
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              12 AA;
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AAY78038
ID AAY78
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anti-tumour;

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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumou urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                Human lactoferrin derived peptide SEQ ID NO:47.
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AAY78047 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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                                           AAY78047;
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Pred. No. 0.00095;
1; Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.3
Matches 10; Conservative
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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AAY 38
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Dolphin GT;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferzin. The peptides are taken up in the intestine through binding to specific lactoferzin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for traating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as uncorant), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferzin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferzin would canble them to be used for the same purposes as lactoferzin at lower
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Pred. No. 0.00095;
1; Mismatches 1; Indels
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Best Local Similarity 83.3
Matches 10; Conservative
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ID AAY7
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RESULT 7 AAY78047

WO200001730-A1.

Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferzin. The peptides are taken up in the intestine through through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used of trush as infant formula food. The peptides can also be used of the food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also be though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                      Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant.formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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Pred. No. 0.00095;
1; Mismatches 1; Indels
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98SE-0004614.
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                                                                                                                      pactericidal; preservative
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Best Local Similarity 83.3.
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                                                                                                                                                                                                                 Synthetic
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AAY78037
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as unimary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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83.3%; Pred. No. 0.001;
cive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                              Dolphin GT;
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                                                                                                                                                                                                                                                                                Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 70; 102pp; English.
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ID AAY78048

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AC AAY78048;

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C AAY78048;

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DT 25-APR-2000 (first entry)

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Fuman lactoferrin derived peptide

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KW

Human, lactoferrin, modification;

KW

food; infant formula; anti-inflaum

KW

wininary tract infection; colitis;

KW

bactericidal; preservative.

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Homo sapiens.

SS

Synthetic.

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WO200001730-A1.

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06-JUL-1999; 99WO-SE01230.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.3
Matches 10, Conservative
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17-JUL-1998;
29-DEC-1998;
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Dolphin GT

Baltzer L,

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Hanson LA, Mattsby-Baltzer I,
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                              Cartoferrin. The peptides are taken up in the intestine through later factoring to specific latchoferrin receptors and are then transported binding to specific latchoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preserved as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Caren though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                     Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:49.
                                                                                   Baltzer L,
                                                                                                                                                                       Claim 15; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78049 standard; Peptide; 13 AA.
                                                                                   Mattsby-Baltzer I,
         98SE-0002441.
98SE-0002562.
98SE-0004614.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.3
Marches 10; Conservative
                                                          (ASCI-) A+ SCI INVEST AB
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         06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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                                                                                   Hanson
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as winheary tract infections, colitis, and Candida Infections (such as winheary, inflammations and/or tumours. The peptides can also be used in food sulfs such as infant formula food. The peptides are also the fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used all initically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 0.001;
1; Mismatches 1; Indels
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                                                                                                                     Claim 18; Page 74; 102pp; English.
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98SE-0004614
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; collitis; Candida infection; fungicidal;
bactericidal; preservative.
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Pred. No. 0.0011;
1; Mismatches 1; Indels
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Claim 12; Page 69; 102pp; English.
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98SE-0002562.
98SE-0004614.
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29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment urinary tract infections, colitis, and Candida infections (such as membrane) inflammations, colitis, and Candida infection on a mucosal membrane) inflammations and/or tunnours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production
urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant foomula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumou
urinary tract infection; colltis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.1%; Score 61; DB 21; Length 14;
83.3%; Pred. No. 0.0011;
ive 1; Mismatches 1; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lactoferrin derived peptide SEQ ID NO:51
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98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 83.3
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                                                                                                                                                                                                                                                                                                                                                                                                                           14 AA;
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.
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                                                                   Query Match 87.1%; Score 61; DB 21; Length 14; Best Local Similarity 83.3%; Pred. No. 0.0011; Matches 10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                         anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-ulcer agent contg. peptide - has low toxicity, is heat-resistant and water-soluble
                                                                                                                                                                                      AAR98554 standard; Peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                    (MORG ) MORINAGA MILK IND CO LID.
                                                                                                                                                                                                                                                    Peptide for anti-ulcer agent.
                                                                                                                                                                                                                                                                                                                                                            94JP-0283869.
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                                                                                                                            3 CFOWORNMRKVR 14
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                                                 14 AA;
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Gaps

; 0

Query Match

87.1%; Score 61; DB 17; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.0012;
Matches 10; Conservative 1; Mismatches 1; Indels

Sequence 15 AA;

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Search completed: February 21, 2003, 07:56:44 Job time: 28.093 secs

The agent is low oln.. It can be

AAR98531-54 are peptides used in an anti-ulcer agent. The a in toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.

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APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NOSUCHI, WATRUU
APPLICANT: NOSUCHI, WATRUU
APPLICANT: TANAKA, SHICERAL
APPLICANT: DOSAKO, SHIW ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: VINTURA, TOSHIAKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
LOCATION: 1.18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM;

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS.

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204,487

FILING DATE: 02-MAR-1994

CLASSIFICATION: 514

ATTORNEY/AGRAT INFORMATION:

NAME: CAMPBELL, PAULA A.

REFERENCE, CAMPBELL, PAULA A.

RESECOMMUNICATION INFORMATION:

TELEPAR, (617) 248-7000

INFORMATION FOR SEQ ID NO. 3:

SEQUENCE, CHARACTERISTICS:

LENGTH: 18 amino acide

TYPE: amino acid

TYPE: ALROWER SEQ ID NO. 3:

SEQUENCE, PAULA A.

READAMATER, PAULA A.

READAM
                                    US-08-724-586-2
US-09-421-632-2
US-08-655-640-2
US-08-655-640-4
US-08-461-333-4
US-08-461-333-4
US-08-461-333-4
US-08-476-798-4
US-08-476-798-4
US-08-476-798-4
US-08-476-798-4
US-08-476-798-4
US-08-476-798-4
US-08-45-681-2
US-08-45-703-2
US-08-464-182A-2
US-08-406-271-2
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                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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Patent No. 5565425
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
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STREET: 53
CITY: BOSTON
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STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-08-204-487-3
Sequence 24, Appl
Sequence 25, Appl
Sequence 24, Appl
Sequence 25, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 7, Appli
Sequence 8, Appli
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                                                                                                                              February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
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Sequence 29,
Sequence 6, A
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Sequence 3,
Sequence 3,
Sequence 1,
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Sequence 8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued Patents AA:*

('GgDZ_6/ptodata/1/iaa/5A_COMB.pep:*
): /GgDZ_6/ptodata/1/iaa/6A_COMB.pep:*
): /GgDZ_6/ptodata/1/iaa/6A_COMB.pep:*
): /GgDZ_6/ptodata/1/iaa/6B_COMB.pep:*
): /GgDZ_6/ptodata/1/iaa/BA_COMB.pep:*
): /GgDZ_6/ptodata/1/iaa/PackfIlesI.pep:*
            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-755-161A-3

US-08-204-487-1

US-08-204-487-1

US-08-256-771-25-

US-08-381-984-25-

US-08-381-984-25-

US-08-381-984-25-

US-09-508-734-6-

US-09-508-734-6-

US-09-508-734-6-

US-09-508-734-6-

US-09-508-734-8-

US-08-204-487-7-

US-09-508-734-8-

US-09-808-734-8-

US-09-808-731-984-29-

US-08-311-984-29-
                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                          262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum March 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                      US-09-743-107B-94
                                                                                                                                                                                                                                                   1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                    score:
                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                               Title:
Perfect
                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No.
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Sequence 8, Application US/08475055
Patent No. 5962245
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STRANDEDDESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFAWKRNMRKVR 12
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GENERAL INFORMATION:

APPLICANT: YONG MING LI

APPLICANT: WISSARA

TITLE OF INVENTION: ENPRODUCTS, AND METHODS OF THEIR USE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE S. 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: AL11 Hackensack

CITY: Hackensack

STRIET: Wew Jersey

COUNTRY: USA
                                                                                                                                             .
0
                                                                                         Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                      Score 61; DB 1; I
Pred. No. 0.00072;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61; DB 2; I
Pred. No. 0.00072;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATVORBY/ABENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELEPRING/DOCKET NUMBER: 947-1-00
TELEFRNENCE/DOCKET NUMBER: 947-1-00
TELEFRNENCE/DOCKET NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08485948
Patent No. 5855882
/ OTHER INFORMATION: (20-37)"
US-08-204-487-3
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Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FRAGMENT TYPE: internal US-08-485-948-8
                                                                                                                                                                                          1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                               1 CFQWQRNMRKVR 12
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Sequence 8; Application US/08628380
Patent No. 5891341
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LIT YONG MING
APPLICANT: ULASSARA, HELEN
APPLICANT: VLASSARA, HELEN
APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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APPLICANT: YONG MING LI

APPLICANT: ATHERN VISSARA

APPLICANT: ANTHONY CERAMI

TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: ENDERODUCTS, AND METHODS OF THEIR USE

NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Hackenbach
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: APPLI 4, 1996
CLASSIFICATION 514
PRIOR APPLICATION 514
PRIOR APPLICATION 1514
PRIOR APPLICATION 1514
ATORNEY/AGENT INFORMATIO:
NAME: Jackson Esq., David A.
RESERRATION: 1995
TELECOMMUNICATION INFORMATION:
TELEFHONE: 201 487-5800
TELEFHONE: 201 343-1684
TELEFA: 133521
INFORMATION FOR EXQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
WUDT: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.3%; Pred. No. 0.00072
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LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
------- rupormation: thiol group of Cys residue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "thiol group of Cys residue at location 2 connected by disulfide bond with thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.1%; Score 61; DB 1; Length 20;
                                                                                                             US/07/755,161A
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DOCUMENT NUMBER:
FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
                                           SOFTWARE: DisplayWite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755
FILING DATE: 19910905
CLASSIFICATION: 530
FRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
TELEFRAX: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSITION IN GENOME:
CTROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
NAME/KEY: modified site
LOCATION: 2
LOCATION: 2
LOCATION: 7
CTHER INFORMATION: Cys res
OTHER INFORMATION: Cys res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
INFORMATION FOR ESO ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
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JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
SIRET: 20005
                                                                                                                                                                        COMPUTER READABLE FORM:
NUBLUM TYEE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
PLASSIFICATION:
APPLICATION NUMBER: 08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION TOWNER: 08/488,217
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 947-1-(
TELECOMMUNICATION INFORMATION:
TELETAX: 201 343-1684
TELETAX: 201 487-5800
TELETAX: 201 343-1684
TELEC CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID MO: 8:
SECTION FO
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8
                                                                                                                          New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFAWKRNMRKVR 12
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                                                                                         CITA.
STATE: Ne.
COUNTRY: USA
70. 07601
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qq 8

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DEMINITY OF 12.

DEMINITY OF 12.

DEMINITY OF 12.

OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cyg residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cyg residue at location 19"

NAME/KEY: modified site
LOCATION: 19

IDENTIFICATION WETHOD: OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: thiol group of OTHER INFORMATION: thiol group of Cyg residue at location 2"

AUTHORS: AUTHORS.

AUTHORS: TITLE: TITLE: TITLE: TITLE: TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: ENAMASAI, YOSHIHIRO
APPLICANT: KAWASAI, YOSHIHIRO
APPLICANT: KAWASAI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIAKI
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: B
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR ADMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61; DB 1; Length 20;
Pred. No. 0.00079;
1; Mismatches 1; Indels
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NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMUTUICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES:

DATE:
DOCUMENT NUMBER:
FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
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Patent No. 5565425
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YAMAMOTO, NAOKI
NAKASHIMA, HIDEKI
MOSUCHI, WATARU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CPAWKRNMRKVR 12
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VOLUME:
ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-08-204-487-1
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                                                   Gaps
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                                              Indels
                                                                                                                                                                                                                                                                                                      RESULT 6
US-07-891-174-3
is Sequence 3, Application US/07891174
is Patent No. 5317084
is REMERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITILE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
in UNDERS OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
is CITE in Manington
Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.25 inch, 500Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 50 COMPUTER: IDEN COMPAGATION COMPUTER: DIS COMPAGATION CYGEN: MS-DOS SOFTWARE: DISPLAYWRITE CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174 FILING DATE: 29-MAY-1992 CLASSIFICATION WUMBER: US 07/755,161 FILING DATE: 05-SEP-1991 ATTORNEY/AGENT INFORMATION: NAME: WALFEN MACHER: MATCH M. CHECK JF. REFERENCE/DOCKET NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECHONICALION INFORMATION: TELECHONICALION INFORMATION INFORMATION: TELECHONICALION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEO ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITS:
FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                              1 CFAWKRNMRKVR 12
                                                                                                                                                                  2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POSITION IN GENOME;
CHROMOSOME/SEGMENT
MAP POSITION;
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20005
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Gaps
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Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mancru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                       ·.
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25
                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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                                                                     87.1%; Score 61; DB 1; 1
83.3%; Pred. No. 0.00079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61; DB 1;
Pred. No. 0.00079;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: WESLINGTON
STATE: WESLINGTON
ZIP: 20005
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: ITEM Compatible
OFFRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U1/2 2, 1994
CLASSIFFCATION: 514
PRICATION NUMBER: S14
PRICATION NUMBER:
FILING DATE: ATTORNEY INFORMATION:
REGISTRATION NUMBER:
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fitteenth Street, N.W., #700 CITY: Washington
                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.1%;
83.3%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                     Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 87.1
Best Local Similarity 83.3
Matches 10; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
PEATURE:
                                                                                                                                                                                                  1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                                                    2 CFOWORNMRKVR 13
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                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-256-771-25
      US-08-256-771-24
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US-08-381-984-24
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Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Manoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                                                                                                                           /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IDM Comparible COMPUTER: IDM Comparible COMPUTER: IDM Comparible COMPUTER: Mordperiect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
CLASSFITCATION 122, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
TELEX:
TELE
TELEFAX: (617) 248-7100
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match.
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                        LOCATION: 1.20
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFAWKRNMRKVR 12
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RESULT 12

US-09-508-734-4

Sequence 4, Application US/09508734

SEQUENCENT Semyang Genex Corporation

TITLE OF INVENTION: Useful microorganism thereof

TITLE OF INVENTION: Useful microorganism thereof

TITLE OF INVENTION: Useful microorganism thereof

TITLE OF INVENTION: USO 0139

CURRENT PALICATION NUMBER: PCT/KR99/00373

FRIOR FILING DATE: 1999-07-14

PRIOR PLING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment the PRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 0.00079;
1; Migmatches 1; Indels
                                                                                                           COMPTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPATE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
         805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WAXTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPERCACHONCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
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Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFAWKRNMRKVR 12
         CITY: Washington STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                         : D.C.
RY: U.S.A.
20005
                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
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    LOCATION:
    LOBNITECATION METHOD:
    COTHER INFORMATION: /note= "the specified peptide as well as
    COTHER INFORMATION: peptides including the specified peptide as a fragment thered
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
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LOCATION:
IDENTIFICATION METHOD:
CTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.1%; Score 61; DB 1; Length 20; 83.3%; Pred. No. 0.00079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
Sequence 24, Application US/08381984

Patent No. 5804555

GENERAL INFORMATION:

TITLE OF INTENTION: ANTIOXIDANT

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                              SCHWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: APPLIL 11, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 83.3
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFAWKRNMRKVR 12
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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POSITION IN GENOME:
CHROMOSCME/SEGMENT:
WAP POSITION:
UNITS:
UNITS:
WAP POSITION:

UNITS:
WAP POSITION:

IDENTIFICATION METHOD:
OTHER INFORMATION:
WAP POSITION:
WAP POSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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83.3%; Pred. No. 0.00097;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
TELEPHONE: 202-371-8856
                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acide
TYPE: AMINO ACID
STRANDEDRESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN:
INDIVIDAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09508734
; Patent No. 6423509
; CENERAL INFORMATION:
GENERAL INFORMATION:
MEET NO. 6423509
; TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: Wass for an improvement of the configuration method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: WASS 124
; FILE REFERENCE: PA/SYG/00.13
; FILE REFERENCE: PA/SYG/00.13
; FILE REFERENCE: PA/SYG/00.13
; FILE REFERENCE: 1999-07-14
; PRIOR FILING DATE: 1999-07-13
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24

TAVE: DATE
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US-07-755-161A-10
US-07-755-161A-10
Sequence 10, Application US/07755161A
Sequence 10, Application US/07755161A
Sequence 10, Application US/07755161A
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES: Wenderoth, lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                 Score 61; DB 4; I
Pred. No. 0.00086;
1; Mismatches 1;
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ZIP. 2000B.
ZIP. 2000B.
ZIP. 2000B.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: Diskette, 5.25 inch, 500KD
COMPUTER: Displaymite
OFFRATING SYSTEM: MS-DOS
SOFTWARE: Displaymite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                 87.18;
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Best Local Similarity 83.3
Matches 10; Conservative
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Matches 10, Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                                                                                                            1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                  2 CFQWQRNMRKVR 13
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Search completed: February 21, 2003, 08:04:27 Job time : 8.93023 secs
                                                                                                                                                                                                                                          FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                OTHER INFORMATION: /no
OTHER INFORMATION: Cys
OTHER INFORMATION: thi
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3
Matches 10; Conservative
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CFOWORNMRKVR 15
                                                                                                                                                                                                                            DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                     US-07-891-174-10
                                                                                                                            JOURNAL:
VOLUME:
ISSUE:
                                                                                                                                                                                     PAGES:
DATE:
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LOCATION: 4

LOCATION: 4

LOCATION: 4

LOCATION: A LOCATION METHOD:

OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with

OTHER INFORMATION: thiol group of Cys residue at location 21"
                    Sequence 10, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
STREET: U.S.A.

CITY: Washington
STREE: U.S.A.
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
OFBRATING SYSTEM: M5-DOS
SOFTWARE: DisplayWite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION NUMBER: US/07/891,174
FILING DATE: 05-RAY-1992
RIOR APPLICATION NUMBER: US/07/55,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M Cheek Jr.
REGISTRATION NUMBER: 33,367
REJECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified site
21
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HARLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
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MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
              07-891-174-10
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/note= "thiol group of Cys residue at location 21 connected by disulfide bond with thiol group of Cys residue at location 4"
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Pred. No. 0.00097;
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Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
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Appli
Appli
2, Appli
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Sequence 20, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 3, Appli
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                                                                                                    February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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Sequence 4, Ap
Sequence 22, A
Sequence 119,
Sequence 119,
Sequence 119,
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Sequence 24,
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1. cgn2_6/ptodata/2/pubpaa/NSO6_NEW_PUB.ppp:*

1. cgn2_6/ptodata/2/pubpaa/NSO6_NEW_PUB.ppp:*

1. cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*

1. cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.ppp:*

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1. cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.ppp:*

1. cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.ppp:*

1. cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.ppp:*

1. cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.ppp:*

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1. cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*

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1. cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*

1. cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-798-869-20
US-09-798-869-6
US-09-798-869-3
US-09-798-869-3
US-09-798-869-3
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US-09-798-89-119
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US-09-798-119-119
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US-09-981-649A-24
                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                           156504 seqs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                1 CFAWKRNMRKVR 12
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Match Length
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Perfect score:
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                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                        Run on:
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Sequence 3574. A Sequence 1248, Ap Sequence 1248, Ap Sequence 5715, Ap Sequence 50, Appl Sequence 11, Appl
                                                                            Sequence 41002, A
Sequence 7, Appli
Sequence 8, Appli
Sequence 29, Appli
        Sequence 30,
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Sequence 38,
Sequence 38,
Sequence 38,
Sequence 38,
Sequence 38,
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0 US-09-981-649A-30

0 US-09-981-649A-32

0 US-09-981-649A-28

0 US-09-98-66-9

US-09-798-869-8

US-09-798-869-8

US-09-798-869-30

US-09-798-869-30

US-09-798-869-30

US-09-798-869-30

US-09-798-869-30

US-09-798-869-30

US-09-10-32-68

US-10-128-049-38

US-10-121-049-38

US-10-121-049-38

US-10-121-049-38

US-10-176-91-38

US-10-176-91-38
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83.3%; Pred. No. 0.00026;
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGHED SYENDEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: ARADUR SYENDAL
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPREMENCE: A3404-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
SPIOR FILING DATE: 1999-08-31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
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1013
1013
1013
1013
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ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFAWKRNIMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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US-09-798-869-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-798-869-2
          Query Match
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APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON

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Gaps
                                                             Gaps
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US-09-798-869-6
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0
Score 61; DB 9; Length 694;
Pred. No. 0.01;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 9; Length 15;
Pred. No. 0.0056;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-798-869-3
US-09-798-869-3
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN GIGURD SVENDSEN
APPLICANT: JOHN GIGURD SVENDSEN
APPLICANT: AREADAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION UNMER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: GIGURG SPEING PRIOR APPLICATION NUMBER: GIGURG SPEING PRIOR PLING DATE: 1998-08-11
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-08-14
PRIOR FILING DATE: 1998-08-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRANKERE FRA
                                                                                                                                                                                                                                                                                                              75.7%;
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54.5%;
      Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                                                        1 CFAWKRINMRKVR 12
                                                                                                                                                             22 CFQWQRNMRKVR 33
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Best Local Similarity
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ORGANISM: CAPRINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-798-869-3
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Patent No. US20020160941A1

GENERAL INFORMATION:

APPLICANT: Kruzel, Tomasz

APPLICANT: Kurecki, Tomasz

APPLICANT: Colinick, Paul D.

APPLICANT: Doyle, Darrell J.

TITLE OF INVENTION: Cloning, Expression, and Uses of Human

TITLE OF INVENTION: Lactoferrin

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price, Holman & Stern

STREET: 400 Seventh &t. N.W.

COUNTRY: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEN COMPUTER:
COMPUTER: BEN FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: Patentin Release #1.0, Version #1.25
CURRATT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 9; I
Pred. No. 0.00043;
1; Mismatches 1;
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A;
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSELSEQ for Windows Version 4.0
SSOFTWARE: 25
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APPLICATION NUMBER: US/08/724,586
APPLICATION NUMBER: US/08/224,586
APPLICATION NUMBER: US/08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E
REGISTRATION NUMBER: 31,409
REFINENCE/DOCKET NUMBER: 31,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 694 amino acids
amino acid
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CFQWQRNMRKVR 14
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CLASSIFICATION:
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

MILEANIUM Pharmaceuticals, Inc.

APPLICANT:

MILEANIUM PHARMATION:

APPLICANT:

MILEANIUM PRACES

TITLE OF INVENTION:

METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF

TITLE OF INVENTION:

METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF

TITLE OF INVENTION:

METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF

FILE REPERENCE: 38155-20044.00

CURRENT APPLICATION NUMBER: US 60/242,040

PRIOR APPLICATION NUMBER: US 60/242,040

PRIOR APPLICATION NUMBER: US 60/242,038

PRIOR APPLICATION NUMBER: US 60/241,992

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: US 60/241,992

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

MUMBER OF SEQ ID NOS: 37

SOFTWARE: PESESEQ for Windows Version 4.0

SEQ ID NO 11

MUMBER: US 001
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Pred. No. 10;
2; Mismatches
                                                                                                 OR FILING DATE: 1999-09-30
OR APPLICATION NUMBER: 09/471,179
OR APPLICATION NUMBER: 09/471,179
OR APPLICATION NUMBER: 09/474,071
OR FILING DATE: 1999-12-29
OR APPLICATION NUMBER: 09/474,072
OR APPLICATION NUMBER: 09/514,010
OR FILING DATE: 2000-02-25
OR APPLICATION NUMBER: 09/516,745
OR FILING DATE: 2000-03-18
OR APPLICATION NUMBER: 09/516,745
OR FILING DATE: 2000-03-14
OR APPLICATION NUMBER: 09/512,002
OR APPLICATION NUMBER: 09/572,002
OR APPLICATION NUMBER: 09/572,002
OR APPLICATION NUMBER: 09/572,002
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                             PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/40
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-29
PRIOR PELICATION NUMBER: 09/47
PRIOR FILING DATE: 1999-12-29
PRIOR PELING DATE: 1999-12-29
PRIOR PELING DATE: 09/51
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/51
PRIOR FILING DATE: 2000-02-19
PRIOR FILING DATE: 2000-02-19
PRIOR FILING DATE: 2000-05-19
PRIOR PILING DATE: 2000-05-19
PRIOR PILING DATE: 2000-05-19
PRIOR PILING DATE: 2000-05-19
PRIOR PILING DATE: 2000-05-29
PRIOR PILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
LENGTH: 333
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Best Local Similarity 54.5
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFAWKRNIMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-26
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       Gaps
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JOS27998A1

LThN: Sean A.

LION: SESTETED PROTEINS AND USES THEREOF

LEICATION NUMBER: US/09/796,753

FILING DATE: 2001-03-01

APPLICATION NUMBER: 09/123,034

FILING DATE: 1998-10-30

AND APPLICATION NUMBER: 09/223,546

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1999-0-26

PRIOR PILING DATE: 1999-0-26

PRIOR FILING DATE: 1999-0-26

PRIOR PILING DATE: PRIOR DATE: PRIOR PILING PILING DATE: PRIOR PILING PIL
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       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
62.9%; Score 44; DB 9;
Best Local Similarity 54.5%; Pred. No. 0.28;
Matches 6; Conservative 3; Mismatches
   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN PERDAL
APPLICANT: BALDUR SVEINBA(RNSSON
APPLICANT: BALDUR SVEINBA(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BLOACITY PERTIDES
CURRENT APPLICATION NUMBER: US/09/798,865
CURRENT APPLICATION NUMBER: US/09/798,865
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSECTION: 25
                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
6; Conservative
                                                                 1 CFAWKRNMRKV 11
                                                                                                                              3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23
   Matches
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CURRENT APPLICATION NUMBER: US/09/978,295A
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Goddard, Audrey
Goddwski, Faul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 119, Application US/09978295A Patent No. US20020156006A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Best Local Similarity 54.5%;
Matches 6; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan, James;
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Ashkenazi, Avi
PPLICANT: Baker Kevin P.
PPLICANT: Botstein, David
PPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFAWKRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-978-295A-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%; Score 40; DB 10; Length 302;
100.0%; Pred. No. 14;
iive 0; Mismatches 0; Indels
                                        57.1%; Score 40; DB 9; Length 301; 100.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.7%; Score 39; DB 9; Length 15; 54.5%; Pred. No. 1.2; 12; wismatches 4; Indels
                                                                                0; Indels
                                                                                                                                                                                                                                         US-09-948-078-2

Sequence 2, Application US/09948078

Sequence 2, Application US/09948078

Patent No. US20020147308A1

GENERAL INFORMATION:
APPLICANT: Holloway, James L.
APPLICANT: Holloway, James L.
TITLE OF INVENTION: Human Vomeronasal Receptor
FILE REFERENCE: 00-73

CURRENT APPLICATION NUMBER: US/09/948,078

CURRENT FILING DATE: 2001-09-06

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 2

LENGTH: 302

LENGTH: 302

TYPE: PART HUMO Sapiens

US-09-948-078-2

US-09-948-078-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: GYSTEIN REKNAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANTON NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTESEQ for Windows Version 4.0
SSOFTWARE: FASTESEQ for Windows Version 4.0
SSOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
                                   Query Match
Best Local Similarity 100.
Matches 6; Conservative
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US-10-080-960-11
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P2630PIC11
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JOS-09-7, SERBOAL-CARLON US/09798869

PUBLICATION NO. US20030022821A1

GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDEN
APPLICANT: YYTEIN REKDAL
APPLICANT: LARS VORLAND
ITILE ROFINFORTION: BIOACTIVE PEPTIDES
ITILE REPERRUCE: A3404-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1996-08-31
PRIOR FILING DATE: 1996-08-31
PRIOR FILING DATE: 1996-08-32
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTUMALE: 25
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PRIOR APPLICATION NUMBER: 09//
PRIOR FILING DATE: 2001-07-30
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PRICES PRICES APPLICATION NUMBER: 60/081955
PRICES FILING DATE: 1998-04-15
PRICES FILING DATE: 1998-04-15
PRICES PELING DATE: 1998-04-12
PRICES PELING DATE

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APPLICANT: Faoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart. Timothy A.
APPLICANT: Stewart. Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William I. Mickey
TITLE OF INVENTION: Scretced and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630911C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 45.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 3; Indels
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PRIOR FILING DATE: 2001-07-30
PRIOR PILING DATE: 1097-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
                     PRIOR FILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08553
PRIOR APPLICATION NUMBER: 60/08553
PRIOR APPLICATION NUMBER: 60/08553
PRIOR APPLICATION NUMBER: 60/08553
PRIOR APPLICATION NUMBER: 60/08557
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
LICATION NUMBER: 60/085582
ING DATE: 1998-05-15
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Gerritsen, Mary E
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čuo, Sophia S.
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Pan, James;
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US-09-978-697-119
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PRICE APPLICATION NUMBER: 60/07763
PRICE PLING DATE: 1998-03-10
PRICE APPLICATION NUMBER: 60/077641
PRICE PLING DATE: 1998-03-11
PRICE PLING DATE: 1998-03-12
PRICE PLING DATE: 1998-03-13
PRICE PLING DATE: 1998-03-13
PRICE PLING DATE: 1998-03-20
PRICE PLING DATE: 1998-03-27
PRICE PLING DATE: 1998-03-31
PRICE PLING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-15
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PRIOR PLING DATE: 1998-04-15
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PRIOR PLING DATE: 1998-04-13
PRIOR PLING DATE: 1998-05-07
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PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
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PRIOR PLIN
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Stewart, Timoth A.

Stewart, Timoth A.

Stewart, Timoth A.

Luna, David L.

Stewart, Timoth A.

"PLICANT: William P. Mickey

APPLICANT: William P. Mickey

TITLE OF INVENTION: Socreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REPRENCY: PSCROOT: PSC
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                           PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR PILING DATE: 1998-05-15
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PRIOR PLING DATE: 1998-05-15
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Patent No. US20020177553A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qlang
Gerber, Hanspeter
FILING DATE: 1998-05-15
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Botstein, David
Desnoyers, Luc
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Best Local Similarity 45.5
Matches 5, Conservative
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PRIOR FILING DATE: 1998-04-21

RRIOR APPLICATION WINERS: 60/08204

RRIOR FILING DATE: 1998-04-22

RRIOR PLILING DATE: 1998-04-28

RRIOR PLILING DATE: 1998-04-29

RRIOR PLILING DATE: 1998-04-28

RRIOR APPLICATION NUMBER: 60/08336

RRIOR APPLICATION NUMBER: 60/083392

RRIOR APPLICATION NUMBER: 60/08339

RRIOR APPLICATION NUMBER: 60/083392

RRIOR APPLICATION NUMBER: 60/083495

RRIOR APPLICATION NUMBER: 60/083495

RRIOR FILING DATE: 1998-04-29

RRIOR PLILING DATE: 1998-05-07

RRIOR PLILING DATE: 1998-05-13

RRIOR PLILING DATE: 1998-05

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APPLICATION NUMBER: 60/080328
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
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R FILING DATE: 1998-04-08
A APPLICATION NUMBER: 60/081049
R FLING DATE: 1998-04-08
A PELING DATE: 1998-04-08
R FLING DATE: 1998-04-08
R FILING DATE: 1998-04-08
R FILING DATE: 1998-04-08
                                                                                                                                                                                                    R FILING DATE: 1998-03-25
R APPLICATION NUMBER: 60/079656
R FILING DATE: 1998-03-26
R FILING DATE: 1998-03-27
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079689
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
APPLICATION NUMBER: 60/082700
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/07939
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079663
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/080107
FILING DATE: 1998-03-31
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LING DATE: 1998-03-31
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G DATE: 1998-04-09
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
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LING DATE: 1998-04-01
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APPLICATION NUMBER: 60/080194
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FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/081952
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     RANGE REPRESENTATION OF SERVICE REPRESENTATI
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ITLE OF INVENTION: Acids Encoding the Same
ILE REFERENCE: P2630P1C63
                                                                                                     Query Match
55.7%; Score 39; DB 9; Length 338;
Best Local Similarity 45.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-999-832A-119
Sequence 119, Application US/0999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Baker, David
APPLICANT: Desnoyers, Luc
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-3
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R APPLICATION NUMBER: 60/077450

R APPLICATION NUMBER: 60/077632

R APPLICATION NUMBER: 60/077632

R FILING DATE: 1998-03-11

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R APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Pani, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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ddard, Audrey
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Kuo, Sophia S.
Napier, Mary A.
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Tumas, Daniel
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PRIOR APPLICATION NUMBER: 60/08299
PRIOR APPLICATION NUMBER: 60/08336
PRIOR APPLICATION NUMBER: 60/08332
PRIOR PLILING DATE: 1998-04-29
PRIOR PLILING DATE: 1998-05-07
PRIOR PLILING DATE: 1998-05-15
PRIOR PLILING DATE:
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Query Match 55.7%; Score 39; DB 9; Length 338; Best Local Similarity 45.5%; Pred. No. 23; Matches 5; Conservative 3; Mismatches 3; Indels

Oy 1 CFAWKRNMRKV 11
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Db 50 CYGWRRNSKGV 60

Search completed: February 21, 2003, 08:11:57 Job time : 6.88372 secs

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ribonucleoside-tri
                                                                 February 21, 2003, 07:48:01 ; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 283224 segs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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                                                                                                                                      1 CFAWKRNMRKVR 12
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Match Length
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2: pir2: *
3: pir3: *
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Maximum DB seq
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Perfect score:
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hypothetical prote	33.3K hypothetical	cell cycle arrest	hypothetical prote	ADP, ATP carrier pr	hypothetical prote	Tl4P4.7 protein -	outer capsid prote	hypothetical prote	protein F21H11.2 [	hypothetical prote	hypothetical prote	hypothetical prote	merTA protein, 12.	probable ribose 5-	hypothetical prote
A84686	G86403	A39654	T32831	G71633	T01179	E86156	A45687	T04555	D88450	E91097	A85943	QQEBHT	\$09523	AH0157	G98020
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236	289	306	413	200	502	513	749	842	2700	235	235	116	116	236	283
52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.1	52.1	51.4	51.4	51.4	51.4
37	37	37	37	37	37	37	37	37	37	36.5	36.5	36	36	36	36

## ALIGNMENTS

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Incorporate names; lactoforus (validated) - human

NALCERAGE STATE (ALTERNATION OF ALTERNATION O
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Gaps

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4; Indels

Length 511

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3-deoxy-manno-octulosonate cytidylyltransferase (EC 2.7.7.38) [similarity] - Helicoba. C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 28-Jul-2000
C;Accession: E64539
C;Accession: E64539
C;Accession: E64539
C;Accession: E64539
C;Accession: E64539
C;Accession: E64539
C;Berance (EC 2.7.7.38)
C;Date: 09-Aug-1997 #text_change 28-Jul-2000
C;Accession: E64539
C;Accession: E64520; MUID: Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, A;Accession: E64539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: 102223
R;Le Provost, P.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Blophys. Res. Commun. 203, 1324-1332, 1994
A;Mitle: Characterization of the goat lactoferrin cDNA: assignment of the relevant lo A;Accession: UC2323; MUID:94380047; PMID:8093048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-393 <TOM> A;Residues: 1-393 <TOM> A;Residues: GB:AE000604; GB:AE000511; NID:g2314086; PIDN:AAD08000.1; PID:g231.
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C;Keywords: nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: mRNA
A,Residues: 1-708 <LEP>
C,Superfamily: transferrin; transferrin repeat homology
C,Keywords: duplication; glycoprotein
P;359-696/Domain: transferrin repeat homology <TRH2>
P;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                        A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176 C;Genetics: A;Gene: STX3070
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llarity 45.5%; Pred. No. 6.6;
Conservative 6; Mismatches 0; Indels
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Pred. No. 2.5;
0; Mismatches
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Matches 5; Conserva
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38 CYQWQRRMRKL 48
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              <PAR>
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A;Map position: 3g21-3g23
C;Superfamily: transferrin repeat homology
C;Superfamily: transferrin repeat homology
C;Superfamily: transferrin #status predicted <51G>
F;1-19/Domain: signal sequence #status predicted <51G>
F;2-0.711/Product: lactotransferrin #status experimental <MAT>
F;20.711/Product: lactotransferrin repeat homology <TRH1>
F;30-56/Domain: transferrin repeat homology <TRH2>
F;30-69/Domain: transferrin repeat homology <TRH2>
F;39-66;39-56;135-218,777-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status eristone file: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0858
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gara, P.
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Atthors: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: protein "Notein "Notein
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A; Molecule type: mRNA
A; Residential type: mRNA
A; Residential source: normal breast tissue
R; Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Eur. J. Biochem. 145, 559-666, 1984
A; Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A; Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                             띹
                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residules: 436-487, 4, 489-711 <RAD>
A; Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
R; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyth A; Tetle: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyth A; Reference number: A61169; MUID:91235214; PMID:1674448
R.Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A.Fitle: Isolation of lactoferrin cDNA from a human myeloid library and expression of
A.Reference number: S07160; MUID:88001031; PMID:3477300
A.Accession: S07160
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A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: A61169
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C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Datcession: B82921
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a m
A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DWA
A;Moledues: 1-386 «GLA»
A;Residues: 1-386 «GLA»
A;Cross-references: GB:AE002120; GB:AF222894; NID:g6899167; PIDN:AAF30624.1; GSPDB:GN0
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jul-1999
C;Accession: D33876
R;Kodelja, V.; Lucas, K.; Barnert, S.; von Kleist, S.; Thompson, J.A.; Zimmermann, W. J. Biol. Chem. 264, 6906-6912, 1989
A;Title: Identification of a carcinoembryonic antigen gene family in the rat. Analysis A;Reference number: A33876; MUID:89214106; PMID:2708349
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hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupon: C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AH3147
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A;Cross-references: GB:M60026; NID:g203407; PIDN:AAA40911.1; PID:g554427; GB:J04626; G
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term
                                                                                                                                                                                                                                                                                                                                                                        serine/threonine kinase UU216 [imported] - Ureaplasma urealyticum
                                                                              Length 267;
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                                                                                                                              3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 2;
Pred. No. 10;
2; Mismatches
                                                                                 .,
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(7
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                                                                           Score 40; DB 2
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.7%;
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                                                                           57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.5
                                                                           Query Match 57.1
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                     158 CFGKKENMRQMR 169
                                                                                                                                                                                 1 CFAWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFAWKRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| | :||:
42 FAWYRGLRKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Genetics:
A,Gene: pkn; UU216
A,Genetic code: SGC3
C,Genetics:
A,Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: B82921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Accession: CG4325
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T. 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUD:20504483; PMID:11016950
A;Accession: C94325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Mycoplasma capricolum
C;Date: 09-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-Dec-1999
C;Accession: S77802
R;Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;
Mol. Microbiol. 16, 955-967, 1995
A;Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiolo
A;Reference number: S77739; MUID:96059641; PMID:7476192
                                                                   C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qan, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and Characterization of sheep lactoferrin, an inhibitor of platelet A;Reference number: S52107; MUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Accession: $77802
A Status: nucled add sequence not shown; translation not shown
A; Status: nucled add sequence not shown; translation not shown
A; Residues: 1-267 <BOR>
A; Cross-references: EMBL: 233006
A; Experimental source: ATCC 27343
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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A;Woldcule vype: DNA
A;Reidus: 1-584 <STO>
A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lypothetical protein MC003 - Mycoplasma capricolum (fragment)
                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-33 <QIA>
C;Superfamily: transferrin; transferrin repeat homology
C;Reywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%; Score 41; DB 2;
45.5%; Pred. No. 1.5;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 2;
Pred. No. 21;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41...,
5, Conservative
                                                     - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                                                              A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-33 <QIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: |: ||: CYQWQKKMRKL 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 5
                                                     actoferrin
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Length 206;

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Cispecies: Brucella melitensis
Cipate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
Cipate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
Cipate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
FibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
J. Mall. Acad. Sci. U.S.A. 99, 443-448
Aritle: The genome sequence of the facultative intracellular pathogen Brucella melit
Arecession: AG3441
Arecession: AG341
Arecession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - Brucella melitensis
         A;Molecule type: DNA
A;Residues: 1-206 <KUR>
A;Residues: GE:AE008688; PIDN:AAL41776.1; PID:G17739129; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 2;
Pred. No. 18;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: I
C;Superfamily: pyridoxamine-phosphate oxidase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                     A.Gene: pdxH
A.Map position: circular chromosome
C.Superfamily: pyridoxamine-phosphate oxidase
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Best Local Similarity 58.3°
The Track Ti Conservative
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C; Species: Agrobacterium tumefaciens
C; Date: 11.-Jan-2002 #sequence_revision 11.-Jan-2002 #text_change 01-Feb-2002
C; Accession. AB2670
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2.317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Krantero, P.; Zhang, S. Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (stric'species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: H97451
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Du
                                                                                                                                                                                                                     ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
A,Accession: A1147
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A, Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A, Reference number: AB2577; PMID:11743193
A, Accession: AB2670
A, Status: preliminary
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-121 <KUR>
A,Cossidues: 1-121 <KUR>
A,Coss-references: GB:AE008689; PIDN:AAL45598.1; PID:g17743317; GSPDB:GN00187
A,Experimental source: strain C58 (Dupont)
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Pred. No. 18;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.5%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 3; Indels
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A;Map positIon: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: linear chromosome
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Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: Atu4804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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Matches
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Gaps

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4; Indels

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C. Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C; Accession: 72597
C. Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C; Accession: 72597
C. R. Dobbson, R.
R. Pobson, R.
R. A. Reference number: 219587
A. Reference number: 219587
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Residues: 1-275 < Will.>
A. Status: Preliminary; translated from GB/EMBL/DDBJ
A. Cross-references: EMBL: Z81089; PIDN: CAB03137.1; GSPDB: GN00028; CESP: F53H4.4
A. Experimental source: clone F53H4
C. Genetics:
A. Canon. Cont. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: CESP:F53H4.4
A,Map position: A,A.
A,Introns: 67/1; 153/1
C,Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 275; 24;
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Best Local Similarity
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262 FQWKISMRKTR 272
2 FAWKRNMRKVR 12
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0; Gaps

3; Indels

1; Mismatches

7; Conservative

Matches

Pycochetical protein MYPU 5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C.Species: Mycoplasma pulmonis
C.Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001
C.Accession: F90580
S.Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A.Fitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A.Reference number: A99512; MUID:21267165; PMID:11353084
A.Accession: F90580
A.Accession: F90580
A.Accession: F90580
A.Accession: F80580
A.A

A;Gene: MYPU 5500 A;Genetic code: SGC3

Gaps ; 55.7%; Score 39; DB 2; Length 282; 50.0%; Pred. No. 24; ive 4; Mismatches 1; Indels Query Match
Best Local Similarity 50.0
Matches 5; Conservative

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Search completed: February 21, 2003, 08:02:48
Job time : 10.6047 secs

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                                                                                                    February 21, 2003, 07:28:06; Search time 5.2093 Seconds (without alignments) 95.544 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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36	34	48	و	1179		ATX1 ARATH	Q91t02	arabidopsis
37	34	48.	9.	1293	-4	XPC DROME	024595	drosophila
38	34	48	و	1574	-	RPOC AQUAE	067763	aquifex aeo
39	34	48.	9.	1576	-	RPOC_AQUPY	Q9×6y2	aquifex pyr
40	34	48	9	1592	~1	YHD5 YEAST	P38735	saccharomyc
41	34	48	؈	1696	<b>~</b>	ITN2 HUMAN	Q9nzm3	homo sapien
42	34	48.	y.	2273	-	ABCR_HUMAN	P78363	
43	34	48.	9	4568	-	DYHB CHLRE	039565	chlamydomon
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45	33	47.	н.	49	н	YIM9_BPPH1	P10432	bacteriopha
						ALIGNMENTS		
RESULT 1								

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Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea
                                                                                                                                                                       21-UUL-1986 (Rel. 01, Created)
15-UUL-1999 (Rel. 38, Lat sequence update)
15-UUR-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Contains: Lactoferroxin A;
Lactoferroxin B; Lactoferroxin C].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Mammary gland;
MEDLINE-90384839; PubMed=2402455;
Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB=Mammary gland;
Liang Q., Jimenez-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Bone marrow;
Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region DNA
                                                                    TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16785; Q16789; O00756; Q9H1Z3; Q96KZ4;
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TISSUE-Mammary gland;
TOSONG H., Chen X., Huan L.;
"CDND A. Cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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TISSUE=Prostate;
Strausberg R.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conneely O.M.; Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
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TISSUE=Mammary gland;
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SECURNCE OF 237-711 FROM N.A.
MCCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansaria A., Mardis E., Schutz K.,
Ghoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis
and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                        "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.",
                                                                                                                                                                                                         MEDLINE-82046817; PubMed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                               SEQUENCE OF 609-711.
MEDLINE=82262043; PubMed=7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-253 -- methionine mutant."; Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                              SECURNCE OF 436-711 FROM N.A.
MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987).
                                                                                                   MEDIINE-85076667; PubMed-6510420;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrine.";
Eur. J. Biochem. 145:659-666(1984).
                                                                                                                                                                                            PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haridas M., Anderson B.F., Baker E.N.; "Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sagripanti J.L.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                An 88 amino acid long C-terminal sequence of human
             TISSUE-Mammary gland;
MEDLINE-90326549; PubMed=2374734;
Powall M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
Nucleic Acids Res. 18:4013-4013 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 670:243-254(1981).
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MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                lactotransferrin.";
?EBS Lett. 142:107-110(1982).
  SEQUENCE OF 3-711 FROM N.A.
                                                                                         SEQUENCE OF 20-711.
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PR. Sun X.L., Baker E. H.M., Sharry S.C., Janeson G.B., Baker E.N.;

R. Acte Crytuallogr. D S:403-407(1999).

R. Acte C
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SIDIAL STILL SET STATEMENT STATEMENT STATEMENT SUBMITTED SUBMITTE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-Somali; TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
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BENBL; AF166879; AAF82241.1; -.
HSSP; O77811; 1B1X.
INTEXPRO; IPRO1156; Transferrin.
Pfam; PRO0405; transferrin; 2.
PRINTS; PRO0422; TRANSFERRIN.
SMART; SMO0094; TR FER, 2.
PROSITE; PSO0206; TRANSFERRIN.1; 2.
PROSITE; PSO0206; TRANSFERRIN.2; 2.
PROSITE; PSO0206; TRANSFERRIN.3; 2.
PROSITE; PSO0207; TRANSFERRIN.3; 2.
PROSITE; PSO0207; TRANSFERRIN.3; 2.
PROSITE; PSO0207; TRANSFERRIN.3; 2.
             Score 61; DB 1; Length 711; Pred. No. 0.0015; 1; Mismatches 1; Indels
                                                                                                                                                                                                                  TRFL CAMDR STANDARD; PRI; 708 AA. O9TUÑO; 09MZS5; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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LACTOTRANSFERRIN
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=MB4 / JCM 11007;
STRAIN=MB4 / JCM 11007;
STRAIN=MB4 / JCM 11007;
STRAIN=B44 / JCM 11007;
STRAIN=B44 / JCM 11007;
STRAIN=Z1992816, PubMed=11997336;
STRAIN=Z1 TAIN Y., IN Y., IN Y., IN Y., Huang L., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700 (2002).
--- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                    Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaces; Thermoanaerobacter.
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE013107; AAM24713.1; -.
Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                         Rel. 41, Last sequence update)
Rel. 41, Last annotation update)
protein L28.
                                                                               (Rel. 41, Created)
(Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 77.8
Matches 7; Conservative
                                                                               15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Interpro; Incorp.

Pfam; Pro0405; transferrin; 2.

PRINTS; PR00422; TRANSFERIN.

BMART; $800045; TRANSFERIN.

PROSITE; PS00206; TRANSFERIN_1; 2.

PROSITE; PS00206; TRANSFERRIN_2; 2.

PROSITE; PS00207; TRANSFERRIN_3; 2.

Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.

Signal.

1 19 BY SIMILARITY.
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Pred. No. 1.9;
3; Mismatches 2; Indels
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Q -> K (IN REF. 2).
F -> P (IN REF. 2).
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F -> P (IN REF. 2).
D -> G (IN REF. 2).
F2EDA3C83539960D CRC64;
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-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN
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EMBL; X78902; CAAS5517.1; -.
HSSP; O77698; ICE2.
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Similarity 54.5%;
6; Conservative
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708 AA;
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57.1%; Score 40; DB 1; Length 62; 77.8%; Pred. No. 0.81; ive 1; Mismatches 1; Indels

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                               STRAIN=ATCC 27343 / KID;
MEDLINE=96059641; PubMed=7476192;
MEDLINE=96059641; PubMed=7476192;
Bork P., Ouzounis C., Casari G., Schneider R., Sander C.,
BOAT M., Gilbert W., Gillevet P.M.;
"Exploring the Myroplasma capricolum genome: a minimal cell reveals
its pbysiology";
Mol. Microbiol. 16:955-967(1995).
-! - SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL (E.COLI) / YCSE/YXEH
(B.SUBFILLS) FAMILY.
                                                                                                                                                                                                Mycoplasma capricolum,
Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
Entomoplasmataceae.
                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                  STANDARD;
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28 WKPNIRKVR 36
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Gaps

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695 AA;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- FUNCTION: TRANSFERRING ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USDIALLY BICARBONATE.

-1- SUBGINIT: MONOMER.

-1- SUBCELLULAR LOCATION: Secreted.

-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                             267 267 267 267 267 AA; D5912DD5B39A8451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                          InterPro; IPR001454; Hlgnase/hydrlase.
InterPro; IPR000150; Hypothet_cof.
Pfam; PF00702; Hydrolase; 1.
PROSITE; PS01228; COF_1; 1.
PROSITE; PS01229; COF_2; 1.
Hypothetical protein.
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PDB; 1B7U; 02-FEB-99.
PDB; 1B7Z; 02-FEB-99.
ILHCEPTC; 1PR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
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nes 7; Conservative
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077811;
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DR SMART; SM00094; TRANSFERRIN.

DR PROSITE; P800205; TRANSFERRIN.

DR PROSITE; P800205; TRANSFERRIN.

DR PROSITE; P800200; TRANSFERRIN.

DR PROSITE; P800200; TRANSFERRIN.

RW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;

FT NON TER 1

T SIGNAL 1

T CHAIN 7

T PROSITE: P800200; TRANSFERRIN.

T PRON TER 1

T PROSITE: P1

T PROSITE: P1

T PROSITE: P2

T PROSITE: P2

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T PROSITE: P4

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Pred. No. 9.9;
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ANION (BY SIMILARITY).
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N-LINKED (GLCNAC. .)
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IRON 2 (BY SIMILARITY).
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Gastrula zinc finger protein XFG20-1 (XLCGF20.1)
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Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse
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                                   uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987)
                                                                                                                                                                                                                                            SEQUENCE OF 1-14 FROM N.A. MEDLINE=9204209; Pubmed=1939212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moriishi K.;
Submitted (NOV-1996)
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                     SEQUENCE FROM N.A.
                                                                                                     TISSUE=Uterus;
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                               MEDLINE=90040698; PubMed=2509712;
Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.
Poeting A., Knoechel W.;
                                                                    Poeting A., Knoechel W.; "Second-order repeats in Xenopus laevis finger proteins."; J. Mol. Biol. 208:639-659(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.7%; Score 39; DB 1; Length 675; 85.7%; Pred. No. 15; 1. Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                             HSSP, P08046; JAII.
TRANSPAC; T02366; ZAII.
TRANSPAC; T02366; ZAII.
TRANSPAC; T02366; ZAII.
FEAM; PF00096; ZAII.
PRINTS; PR00049; ZINCFINGER.
PRODOM; PD000003; ZAII. CZHZ; SIII.
PROSTIE; PS00029; ZINC_FINGER.
PROSTIE; PS001029; ZINC_FINGER.
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TISSUE-Uterus;
MEDLINE-87280033; PubMed=3611056;
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                  85-613 FROM N.A.
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nes 6; Conservative
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TRFL MOUSE
TO TRPEL MOUSE
DT 01-AUG
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DT 15-UUN
DT 15-UUN
DT 15-UUN
DT 16-UUN
DT 18-UUN
DT 18-UUN
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                                                                                                                                                                                                                                                                                                      Liu Y., Teng C.T.;

"Chazacterization of estrogen-responsive mouse lactoferrin promoter.";

"Chazacterization of estrogen-responsive mouse lactoferrin promoter.";

"I slol. Chem. 26:21880-21885(1991).

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION. USUALLY BICARBONATE.
-!- SUBUNIT: MONOMER.
-!- SUBJUNIT: MONOMER.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J03299; AAA40525.1; -...
R BMBL; D88510; BAA13633.1; -...
R BMBL; M74778; AAA39427.1; -...
R BMBL; M74778; AAA39427.1; -...
R BMBL; M74778; AAA39427.1; -...
R FARSP; P02788; LUEE.
R M2D; M2I:96837; LLf.
R InterPro; IPR001156; Transferrin.
R Pfam; PP00405; TRANSFERRIN.
R PROSITE; PS00205; TRANSFERRIN.
R PROSITE; PS002006; TRANSFERRIN 1; 1.
R PROSITE; PS002007; TRANSFERRIN 2; 2.
R PROSITE; PS002007; TRANSFERRIN 3; 2.
R PROSITE; PS002006; TRANSFERRIN 3; 2.
R PROSITE; PS002006; TRANSFERRIN 3; 2.
to the EMBL/GenBank/DDBJ databases.
                                                                                                                    Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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LACTOTRANSFERRIN
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us-09-743-107b-94.rsp

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XX MEDLINE=22075758; PubMed=1742360;
XX Kruft V., Kapp U., Wittmann-Liebold B.;
XT "Characterization and primary structure of proteins L28, L33 and L34
The Bacillus stearchharmophilus ribosomes.";
Eliochimie 73:855-860(1991)
C -1- SIMILARITY: BELCONGS TO THE L28P FAMILY OF RIBOSOWAL PROTEINS.
XP INT, A483996, A48396, A83908, R1bosomal L28.
R InterPro; IPRO1383; Ribosomal L28.
R TIGRAMS; TIGRO0009; L28; I.
NR RIBOSOMAL FIGRO009; L28; I.
NR RIBOSOMAL POTCHIN.
TIGRAMS; TIGRO009; L28; I.
NR RIBOSOMAL POTCHIN.
TIGRAMS; TIGRO009; L28; I.
NR RIBOSOMAL POTCHIN.
TINIT MET 0
SEQUENCE 60 AA; 6810 MW; ZAD9161CD60B82F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN MJ0832, 1ST PART (POTENTIAL).
HYPOTHETICAL PROTEIN MJ0832, 2ND PART (POTENTIAL).
(POTENTIAL).
HYPOTHETICAL PROTEIN MJ0832, 3ND PART HYPOTHETICAL PROTEIN MJ0832, 3ND PART HYPOTHETICAL PROTEIN MJ0832, 3ND PART
                                            InterPro; IRR03586; Hedgehog hintc.
InterPro; IRR03587; Hedgehog_hintc.
InterPro; IRR002203; Intein.
InterPro; IRR004042; Intein.
InterPro; IRR004042; Intein.
PFO3477; ATP-cone; 2.
PRINTES, PR00379; INTEIN.
SMART; SM00306; Hintc; 2.
SWART; SM00306; Hintc; 2.
PROSITE; PS50818; INTEIN C TER; 2.
PROSITE; PS50819; INTEIN N TER; 2.
PROSITE; PS50817; INTEIN N TER; 2.
Hypothetical protein; Autocatalytic cleavage; Protein splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 1; Length 1750;
Pred. No. 39;
3; Mismatches 2; Indels
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Pred. No. 1.8;
2; Mismatches 1; Indels
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Bacteria; Firmicutes; Bacillales; Geobacillus.
NCBI_TaxID=1422;
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01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
50S ribosomal protein L28.
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 54.5
---nhes 6; Conservative
                    InterPro; IPR005144; ATP
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1750
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RL28_LISMO
ID _RL28_LISMO
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P23374;
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RI28_BACST
IN TABLES
BAC P23374
DT 01-NOV
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DE SOS Bacill
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CO BACTER

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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=9633799; PubMed=6688087;
MEDLINE=9633799; White O. Olsen G.J. Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb-J.-F., Adams M.D., Ratch C.I.,
Coverbeek R., Kirkness E.F., Weinstook K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodowsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN) FOLLOWED BY PEPTIDE LIGATION (POTENTIAL).
-!- SIMILARITY: WEAK IN THE C-TERMINAL, TO M.JANNASCHII MJ0885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last annotation update)
Hypothetical protein MJ0832 (Contains: Mja rnr-1 intein; Mja rnr-2 intein)
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (POTENTIAL).
ALINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
MR -> IQG (IN REF. 1).
R -> Q (IN REF. 2).
M -> L (IN REF. 2).
S -> T (IN REF. 2).
S -> T (IN REF. 2).
E -> Q (IN REF. 1).
E -> G (IN REF. 1).
E -> G (IN REF. 1).
C -> U (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 1; Length 707;
Pred. No. 15;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococales;
Methanocaldococaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U67527; AAB98834.1; -.
HSSP; P17255; IDFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      25
82
359
382
449
429
629
707 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFAWKRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 CLRWONEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIGR: MJ0832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
Y832 METUA
ID Y832 METJA
AC Q58242;
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CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
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METAL
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CARBOHYD
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Gaps

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                                                                                                                                                                                                                                                                       WEDLINE-21385309; PubMed=11493673;
Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fesquet D.,
Johnston L.H.:
"The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
                                                                                                                                                                                                                                                                                                                                                                                 J. Cell Sci. 114:2345-2354(2001).
-1- FUNCTION: Part of a checkpoint which monitors spindle integrity and prevents premature exit from mitosis. This cell-cycle arrest depends upon inhibition of the G-protein Teml by the BFAI/BUB2
MEDLINE=91330299; PubMed=1651171;
Hoyt M.A., Totis L., Roberts B.T.;
S. cerevisiae genes required for cell cycle arrest in response to
loss of microtubule function.";
cell 66:507-517(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Madrid E;
MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae, Rickettsieae; Rickettsia.
NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 306;
Pred. No. 15;
2; Mismatches 3; Indels
                                                                                                                                       SEQUENCE FROM N.A.
STRALM-S288C / ABP72;
Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00164; TBC; 1.
Cell cycle; Mitosis.
SEQUENCE 306 AA; 35027 MW; AIDDBFB548E81EA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP_APP carrier protein 5 (ADP/ATP translocase 5)
TLCE OR TLCS OR RP739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR, A39654; A39654.
SGD; S0004659; BUB2.
InterPro; IPR000195; RabGAP_TBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M64706; AAA16885.1; -. EMBL; Z49703; CAA89765.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
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                                                                                                                                                                                                                                                                                                                                                              regulates cytokinesis."
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Rest Local Similarity
Frace 5; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsia prowazekii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 CFAWOTOORR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFAWKRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      CHARACTERIZATION.
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TLCE RICPR
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                                                                                                                                                                                                                                                                                                                                  Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
A. Charbit A., Chectouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno B., Matcourna A., Mata Vicente J., NG E., Nedjari H.,
A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
BUB2 OR YMR055C OR YM9796.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 1; Length 62;
Pred. No. 1.9;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                 CLIP 11262 / Serovar 6a;
                                                                                                                                                                             Bacteria; Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBL_TaxID=1639, 1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA43DE039213C562 CRC64;
                              5-JUN-2002 (Rel. 41, Created)
5-JUN-2002 (Rel. 41, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 306 AA.
                                                                                                                                                                                                                                                                           SPECIES=L.monocytogenes, and L.innocua;
STRAIN=EGD-e / Serovar 1/2a, and CLIP 1
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00830, Ribosomal L28, I.
TIGRFAMS, TIGR00009, L28, 1.
Ribosomal protein, Complete proteome.
SEQUENCE 62 AA, 6991 MM, AA43DE03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listilist, LIN01930, -.
Listilist, LMO01816; -.
InterPro, IPR001383; Ribosomal L28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL591981; CAC99894.1; -. EMBL; AL596170; CAC97160.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.3%;
                                                                                                                                              Listeria monocytogenes, and
                                                                                                 50S ribosomal protein L28. RPMB OR LM01816 OR LIN1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 WKRNMRKVR 12
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 WKANLOKVR 37
                                                                                                                                                                      Listeria innocua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
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              292AJ2
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BUB2 YEAST
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Best Loca Matches

8 요 REAL COCOS GENERAL BENERAL BEN

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Gaps

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 human group B rotavirus ADRV.";
-1. Virol. 677:2730-2738(1939)
-1. SUBCELLULAR LOCATION: Outer capsid.
-1. SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 1; Length 749; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                       EMBL; M91434; AAA47338.1; -.
InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.9%;
                                                                                                                                                                                                                                                                                                  Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.v.,
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                        133
407
527
568
620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhi, and
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 CFTWDMNCANVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFAWKRNIMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=601, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    749 AA;
                                                                                                                                                                                                                                                                                                                                   Coat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella.
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                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=93233240; PubMed=8386274;
Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.;
"Identification and baculovirus expression of the VP4 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VP4 ROTGA STANDARD, PRT; 749 AA.

004916;

01-UTN-1994 (Rel. 29, Created)

01-UTN-1994 (Rel. 29, Last sequence update)

01-UTN-1994 (Rel. 29, Last annotation update)

outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
"The genome sequence of Rickettsia prowazekii and the origin of mitochondria.",
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Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus)
Viruses; dsRNA viruses; Reoviridae; Rotavirus.

NCBI_TaxID=12705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.9%; Score 37; DB 1; Length 500; 54.5%; Pred, No. 25; 1.00 2; Mismatches 3; Indels ive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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Transmembrane; Transport; ATP-binding; Multigene family;
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                                                                                                           MEDLINE=97419517; PubMed=9274032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, Y11778; CAA72457.1; ...
InterPro; IPR004667; ADP_car.
Pfam; PF03219; TLC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57073 MW;
                                                                        OF 325-500 FROM N.A.
                                     Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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500 AA;
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TRANSMEM 26
TRANSMEM 62
                                                                                          STRAIN-Madrid E;
                                                                          SEQUENCE
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RD SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

RE SEQUENCE S. typhi; STRAIN=CT18; PLASMID=pHCM1;

RX MEDLINE=21534947; PubMed=11677608;

RA PARKHILI J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebathia M.,

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebathia M.,

RA Chain A., Davis R.M., Dowd L., Mitter N., Farrar J.,

RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

RA Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;

RC Willen Serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SECTISS-S.f.laxneri;
MEDLINE=85014891; PubMed=6091128;
Misra T.K., Brown N.L., Fritzinger D.C., Pridmore R.D., Barnes W.M.,
                                                                                                                                                                                                                                                                                 Plasmid pHCM1, and Plasmid IncFII NR1.
Bacteria; Proteobacteria, gamma subdivision, Enterobacteriaceae;
20-WAR-1987 (Rel. 04, Created)
20-WAR-1887 (Rel. 04, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Mercuric transport protein (Mercury ion transport protein)
MERT OR HCM1.234C.
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                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Integral membrane protein, Inner membrane.
Haberstroh L., Silver S.;
"Mercuric ion-resistance operons of plasmid R100 and transposon infold. The beginning of the operon including the regulatory region and the first two structural genes.";
Proc. Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).
                                                                                                                          PRECIES : Ilexneri; PLASMID=IncFII NR1; TRANSPOSON=Tn21; GEDLINE=85159407; PubMed=6530603; Asirineau P., Gilbert P., Jackson W.J., Jones C.S., Summers A.O.,
                                                                                                                                                                                                                      plasmid NR1 ";
J. Mol. Appl. Genet. 2:601-619(1984).
-!- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
FROM THE PERIPLASMIC MERP PROTEIN TO THE NERCURIC REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fam; PF02411; MerT; 1. ransport; Mercury; Plasmid;
                                                                                                                                                                                                 The DNA sequence of the mercury resistance operon of the IncFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 1; Length 116;
Pred. No. 8.3;
1; Mismatches 3; Indels
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HG(2+) (POTENTIAL).
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HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
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InterPro; IPR003457; Transprt_MerT.
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12521 MW;
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EMBL; J01730; AAA92261.1; -.
EMBL; K03089; AAB59075.1; -.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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116 AA;
                                                                                                            SEQUENCE FROM N.A.
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TRANSMEM 16
TRANSMEM 46
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SEQUENCE
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Search completed: February 21, 2003, 07:51:41 Job time : 6.2093 secs

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0927h8 rhizobium m 0897h8 rhizobium m 0897h8 rhizobium m 089790 ceenorhabdi 063112 rattus mercella mer

065237 arabidopsis

044841 caenorhabdi

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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2010 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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TISSUE-PROSTATE;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022347; AAH22347.1; --
SEQUENCE 711 AA; 78327 MW; 1B9C7EB097C45FAF CRC64;
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80.0%; Score 56; DB 4;
Best Local Similarity 81.8%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 1
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Q8YFK3
Q83112
Q93780
Q98Q19
Q8RZA4
Q9RRA4
Q17549
P93833
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Q9UFK6
Q9CA22
O90863
Q98RR2
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Q95K05
Q96GY3
Q9C6N2
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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QBTCD2
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Q9UCYS
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Q8TCD2
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Ogz462 salmonella
O25611 helicobacte
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                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q9UCY5
Q8Z462
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Q9Z611
Q9UZ5
Q9HPA3
Q9HPA3
Q8R9U1
Q9BXW1
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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Maximum DB
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Helicobacter pylori (Campylobacter pylori).
Bacteria; proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
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Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; 077698; 1CE2.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.MXY-2000 (TrEMBLrel. 13,
01-MAX-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 45.
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                                                                                                                                                                                                                                                                                                                                                                Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 FAWKKNIKRIK 120
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Matches 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ovis aries (Sheep
                                                       NCBI_TaxID=210;
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09JJZS;
01-OCT-2000
01-OCT-2000
01-JJN-2002 (
                                                                                                                                                                                                                                                                                                             Venter J.C.;
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094425
ID 09443
AC 09443
DT 01-00
DT 01-00
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                                                                                                  Sato I.;
"Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred. No. 4.4;
0; Mismatches 4; Indels
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                              74.3%; Score 52; DB 4; Length 38; ilarity 81.8%; Pred. No. 0.026; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ll protein, Complete proteome.
511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                        InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8Z462;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 AA
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01-JAN 1998 (TrEMBLrel. 05, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                 Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21534947; PubMed=11677608;
                                                         SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 413:848-852(2001).
EMBL; AL627276; CAD06049.1; -.
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Best Local Similarity 66.7%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                  2 FAWKRINMRKVR 12
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
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NCBI_TaxID=601;
                                                                                                                                     seminal plasma.
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SEQUENCE 51
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RESULT 3 Q8Z462

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RESULT 4 025611 1D 0256 AC 0256 AC 01-J DT 01-J DT 01-D DE 3-de GN HP09

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SEQUENCE FROM N.A.
STRAIN=26655 / ATCC 700392;
MEDLINE=2655 / ATCC 700392;
MEDLINE=37394467; PubMed=252185;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=978, Klenk H.-P., Gill 8., Dougherty B.A., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill 8., Dougherty B.A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne D.D., Utterback T.R., Peterson J.D., Kelley J.M., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
VCBI_TaxID=9940;
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llarity 45.5%; Pred. No. 2;
Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000604; AAD08000.1; -.
TIGR; HP0957; -.
Hypothetical protein; Transferase; Complete proteome.
BSEQUENCE 393 AA; 45622 MW; 6428BA3321554F46 CRC64;
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5, Conservative
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Best Local Similarity
Matches 5; Conserv
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Matches 7; Conser
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Q8R9U1
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Q9BXW1
                          SCREEKS
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MEDLINE=20504483; PubMed=11016950;
MY V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
NG W.V., Kennedy S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swatzell S., Reir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20241927; PubMed=10777661;
Buchner G., Orfanelli U., Quaderi N., Bassi M.T., Andolfi G.;
Buchner G., Orfanelli U., Quaderi N., Bassi M.T., Andolfi G.;
"Identification of a new EdF-repeat-containing gene from human Xp22:
Genomics 65:16-23(2000).
-!- SIMILARITY: CONTAINS 1 MAM DOWAIN.
-!- SIMILARITY: CONTAINS 1 MAM DOWAIN.
HSSP; P35555; 1EMN.
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Hypothetical 61.5 kDa protein.

EGFL6 OR W80.

Was musculus (Mouse),

Was mysculus (Actazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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PROSITE; PS00012; BGF_1; UNRNOWN_1.
PROSITE; PS01186; BGF_2; 2.
PROSITE; PS01186; BGF_2; 3.
PROSITE; PS00060; MAM_2; 1.
Calcium-binding; BGF_1 ke domain; Glycoprotein; Hydroxylation; SEQUENCE 550 AA; 61520 MM; DEF936325C9F31B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 11; Length 550;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                       Franco B.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPR0000561; BGF-like.
InterPro; IPR001881; BGF Gomain.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.6%;
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WART; SM00179; EGF CA; 3.

WART; SM00001; EGF like; 2.

WART; SM00137; MAM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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fam; PF00629; MAM; 1.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                           Franco B.
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099JX4;
01-UJN-2001 (TrEMBLrel. 17, Created)
01-UJN-2001 (TrEMBLrel. 17, Last sequence update)
01-UJN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to dendritic cell protein.
Similar to dendritic cell protein.
Buka musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
DJ69B10.1 (GA17 protein) (Hypothetical 42.5 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strauberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL078477; CAC68392.1; -.
InterPro; IPR000717; PCI.
InterPro; IPR000717; PCI.
Hypothetical protein.
SEQUENCE 374 Aa; 42503 MW; 63736CA2B093D794 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cobley V.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Best Local Similarity 60.0
Matches 6; Conservative
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Matches 6; Conserva
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                                             356 AWKONLNKVK 365
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3 AWKRNMRKVR 12
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AC 099UXA
AC 099UXA
DT 01-UU
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Q96KM8
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Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;

"Identification of G protein-coupled receptor genes from the human genome sequence.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB083609; BAB89322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GA17 protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Euklaria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                    57.1%; Score 40; DB 4; Length 206; 60.0%; Pred. No. 20; cive 3; Mismatches 1; Indels
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Zhao Z., Huang X., Li N., Zhu X., Cao X.;
"A novel gene from human dendritic cell.";
Submitted (Max-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFF064603; AAC17108.1;
InterPro; IPR000717; PCI.
Pfam; PF01399; PCI; 1.
SMART; SMO0888; PINT; 1.
SEQUENCE 374 AA; 42512 MW; 2CFF2BCB70F997A7 CRC64;
Pfam; PF01399; PCI; 1.
SMART; SM00088; PINT; 1.
SEQUENCE 206 AA; 23754 MW; 940D5B66271A44B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 AA; 33557 MW; AB7F9792957BFCA6 CRC64;
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01.AUG-1998 (TrEMBLrel. 07, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative G-protein coupled receptor.
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Best Local Similarity 60.0-
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                3 AWKRINMRKVR 12
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STRAIN=BD II; TISSUB=LIVER;
MEDLINE=89214106; PubMed=2708349;
MEDLINE=89214106; PubMed=2708349;
MEDLINE=89214106; PubMed=2708349;
Zimmermann W.A.;
Zimmermann W.A.;
"Identification of a carcinoembryonic antigen gene family in the rat: Analysis of the N-terminal domains reveals immunoglobulin-like, Analyservariable regions.";
J. Biol. Chem. 264:6906-6912(1989).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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MEDLINE-20500219; PubMed=11048724;
Glass J.I., Lefkowitz B.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
"The complete sequence of the mucosal pathogen Ureaplasma
urealyticum.";
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                                                                                                                                                                                                                      Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacceria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Wycoplasmatacae; Ureaplasma.
NCBI_TaxID=134821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%; Score 40; DB 16; Length 386; 54.5%; Pred. No. 39; 21ve 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfan; PF00069; pkinase; I.
ProDom; PD000001; Buk_pkinase; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS01009; PROTEIN KINASE_ST; UNKNOWN 1.
ATP-binding; Transferase; Complete proceedme.
SEQUENCE 386 AA; 45241 MW; 789374CC15D1CAD9 CRC64;
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                                                                                                                       Last sequence update)
Last annotation update)
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Last annotation update)
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Nature 407.757-762(2000).
Nature 407.757-762(2000).
SMBL; AB002120; AR780634.1; -.
Interpro; IPR00019; Euk pkinase.
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01-JAN-1999 (TrEMBLrel. 09, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                  Created)
                                                  PRT;
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                                             O9PQS6 PRELIMINARY;
O9PQS0 (TEMBLE1 15, C1
01-OCT-2000 (TEMBLE1 15, L6
01-MRX-2002 (TEMBLE1. 20, L6
Serine/threonine kinase.
PKN OR UU216.
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Best Local Similarity 54.5
Matches 6; Conservative
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Search completed: February 21, 2003, 08:00:47 Job time : 22.6744 secs Human lactoferrin

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Dolphin

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Baltzer

Anti microbial pep Lactoferrin-relate

AAY68867 AAY78032 AAR21810 AAR44841

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Human, lactoferrin, modification, infection, inflammation, tumour, food; infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.
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98SE-0002562.
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 WPI; 2000-147388/13.
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Synthetic.
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                                                                                                              February 21, 2003, 07:37:21; Search time 28:093 Seconds (without alignments) 56.918 Million cell updates/sec
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              GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

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AAR98553 AAR91852 AAW03045

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                                                                                        AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fundicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                     anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                             Claim 22; Page 38; 102pp; English.
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Best Local Similarity
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AAY78001 to AAY78100 represent peptides having sequences based on human

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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 0.00038;
0; Mismatches 1; Indels
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                                                                                                                                                                                                 AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment or no be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food sulfs such as infant formula food. The peptides are also in food sulfs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a byraid basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                               Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                               Score 62; DB 21; Length 12;
Pred. No. 0.00057;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dolphin GT
                                                                                                                                                                                                                                                                                                                                                          Human lactoferrin derived peptide SEQ ID NO:89.
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                                                                                                                                                                                                                                                                           AAY78089 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Page 37; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanson LiA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                                                                                        bactericidal; preservative
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                        11; Conservative
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                                                                                                                                                                                                          CFAWQRINMRKVR 12
                                                                                                                                                                                  1 CFAWQRAMRKVR 12
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                                                                                                                              Ouery Match
Best Local Similarity
Matches 11; Conserv
                                                                                                       12 AA;
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29-DEC-1998;
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                                                                                                       Seguence
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                                                                                                                                                                                                                                                  RESULT 4
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferin. The peptides are taken up in the intestine through binding to specific lactoferin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as uninearine), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                             Gaps
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  Score 59; DB 21; Length 12;
Pred. No. 0.0018;
Nismatches 2; Indels
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83.3%; Pred. No. 0.0018;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:90.
                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltzer L,
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                                                                                                                                                                                                                                                                                                     AAY78090 standard; Peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mattsby-Baltzer I,
86.8%;
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                                                          10; Conservative
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                                                                                                              1 CFAWQRAMRKVR 12
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                                  Local Similarity
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Best Local Similarity
Matches 10; Conserv
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17-JUL-1998;
29-DEC-1998;
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(first entry)

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Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                               Human lactoferrin derived peptide SEQ ID NO:86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 36; 102pp; English.
AAY78086 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                            Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB.
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                                                                                                                                                                                Homo sapiens.
Synthetic.
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17-JUL-1998;
29-DEC-1998;
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                          AAY78086;
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                                                                                                                                                                                                                     food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dolphin GT;
                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:93.
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                                                                                            AAY78093 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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1 CFAWQRAMRKVR 12
                       1 CFQWQRXMRKVR 12
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17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                 sapiens.
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                                                                                                                                                                                                                                                                                            Synthetic.
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Dolphin GT;

Baltzer L,

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactucidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Best Local Similarity 83.3
Matches 10; Conservative
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0; Gaps

Score 59; DB 21; Length 12; Pred. No. 0.0018; 1; Mismatches 1; Indels

Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative

12

1 CFAWQRAMRKVR

1 CFQWKRAMRKVR 12

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RESULT 7 AAY78086

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uniary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fundicial and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
            Human, lactoferrin, modification; infection, inflammation; tumour;
food, infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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Pred. No. 0.0027;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 38; 102pp; English.
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                                                                                                                                                                                                               98SE-0002441.
98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB.
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                                                                                                                            WO200001730-A1.
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17-JUL-1998;
29-DEC-1998;
                                                                                    sapiens
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 12; Page 70; 102pp; English.

Dolphin GT;

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13.

98SE-0002441. 99WO-SE01230.

WO200001730-A1

Synthetic.

06-JUL-1999;

13-JAN-2000

98SE-0004614

29-DEC-1998;

06-JUL-1998; 17-JUL-1998; (ASCI-) A+ SCI INVEST AB.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for traating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as urinary tract inferences, colitis, and Candida infections a memorane), inflammations and/or tumours. The peptides can also be used in food sruffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Byon though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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Best Local Similarity 83.3
Matches 10; Conservative
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Gaps

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens

Human lactoferrin derived peptide SEQ ID NO:38.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urihary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. It inflammators and many also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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food, infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57; DB 21; Length 12;
Pred. No. 0.0039;
0; Mismatches 2; Indels
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                                                                                                        Baltzer L,
                                                                                                                                                                                                               Claim 15; Page 35; 102pp; English.
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                                                                                                        Hanson LA, Mattsby-Baltzer I,
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98SE-0002562.
98SE-0004614.
                            98SE-0002562.
98SE-0004614.
             98SE-0002441
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                        (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFAWORAMRKVR 12
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17-JUL-1998;
29-DEC-1998;
                            17-JUL-1998;
29-DEC-1998;
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           06-JUL-1998;
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AAY78047
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used as fulfs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also through native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Dolphin GT
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Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY78037 standard; Peptide; 13 AA.
                                                                                                         Claim 18; Page 73; 102pp; English
Hanson LA, Mattsby-Baltzer I,
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98SE-0002562.
98SE-0004614.
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Les 10; Conservative
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                            WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
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29-DEC-1998;
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urinary tract infections, colitis, and Candida infection on a mucosal
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                                                AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food sulfs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Been though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; collitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB 21; Length 13; Pred. No. 0.0042;
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Claim 12; Page 70; 102pp; English
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98SE-0002562.
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17-JUL-1998;
29-DEC-1998;
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membrane), infilammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desirred anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 0.0042;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78049 standard; Peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.8%;
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98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colttis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, lactoferrin, modification; infection; inflammation, tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                 Score 57; DB 21; Length 13; Pred. No. 0.0042; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                         AAY78036 standard; Peptide; 14 AA.
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98SE-0002562.
98SE-0004614.
                                                                                                                 Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                 13 AA;
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29-DEC-1998;
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83.8%; Score 57; DB 21; Length 14;

Query Match

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Gaps
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             Indels
Pred. No. 0.0045;
0; Mismatches 2;
                                                                                                               Search completed: February 21, 2003, 07:56:45 Job time: 29.093 secs
 83.3%;
Best Local Similarity 83.3
Matches 10; Conservative
                                           1 CFAWQRAMRKVR 12
                                                                    3 CFOWORNMRKVR 14
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Gaps

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Sequence
Seq
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APPLICANT: NAKASHINA, HIDEKI
APPLICANT: MOSCHIL, WATARU
APPLICANT: MOSCHIL, WATARU
APPLICANT: DOSAKO, SHIGERAI
APPLICANT: TANAKA, SHIGERAI
APPLICANT: TOSAKO, SHUN'ICHI
APPLICANT: TOSHIAKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SUCHENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02107

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
ATTONARY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFRENCE/DOCKET NUMBER: 32,503
REFRENCE/DOCKET NUMBER: 517,000
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE GARRACTERISTICS:
FURTHER. 18 AMINO ACIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ ADDRESSEE: THIBERULT STREET: 53 STATE STREET CITY: BOSTON STATE:
                                                    US-08-724-586-2
US-09-421-632-2
US-08-655-640-2
US-08-655-640-4
US-08-154-019-4
US-08-154-019-4
US-08-158-313-4
US-08-158-313-4
US-08-145-691-4
US-08-145-691-4
US-08-145-691-4
US-08-145-691-4
US-08-145-691-4
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US-08-456-106-2
US-08-456-108-2
US-09-265-577-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08204487; Patent No. 5565425
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RDNESS: single
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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COUNTRY: USA
ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-204-487-3
  2226666666666444444
800126466666644444
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                                                                                                                                                                                    February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, A Sequence 8, A Sequence 8, A Sequence 3, A Sequence 1, A Se
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Sequence 6, 7
Sequence 6, 7
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/cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
                             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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S-09-508-734-6
S-07-755-161A-10
S-07-891-174-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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68
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Match Length
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Perfect score:
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Maximum DB seq
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                                                                                                                                                                                          Run on:
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1 CFAWORAMRKVR 12
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US-08-475-055-8
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APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                            0
                                                                                     Length 18;
                                                                                                                          2; Indels
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Pred. No. 0.0016;
0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                Score 57; DB 1;
Pred. No. 0.0016;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION NUMBER: 08/488,217
APPLICATION NUMBER: 08/418,642
FILING DATE: 47NE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NUMBER: Jackson Eq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-0
TELEPHONE: 20,1487-5600
TELEPHONE: 20,1487-5600
TELEFAX: 201 343-164
TELEFAX: 201 343-164
TELEFAX: 201 343-168
TELEFAX: 201 343-168
TELEFAX: 201 343-168
TELEFAX: 201 487-5600
TELEFAX: 201 343-168
TELEFAX: 201 343-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATES SEE: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA ZIP: 07601
                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08485948
Patent No. 5855882
;
US-08-204-487-3
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Best Local Similarity 83.3%;
                                                                                Query Match 83.8%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                               1 CFAWORAMRKVR 12
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CFOWORNMRKVR 12

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185-01-80-80
187-01-62-180-9
187-01-62-180-9
187-01-62-180-9
187-01-62-180-9
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FEATURE:
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NAME INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                 NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                           FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys re
OTHER INFORMATION: thiol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                    DisplayWrite
                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGNENT:
WAP POSITION:
UNITS:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Fatent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamory TOWITA et al.
ITILE OF INVENTION: Antimicrobial Peptides and an ITILE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
STREET: D.C.
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 2;
Pred. No. 0.0016;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: JUNE 7, 1995
CLASSIFICATION: NUMBER: 08/418,642
FILING DATE: ARRIL 7, 1995
CLASSIFICATION: ARRIL 7, 1995
CLASSIFICATION: ARRIL 7, 1995
ATDONERY/ABOUT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENNE/ADOKET NUMBER: 947-1-(
TELECHONNICATION INFORMATION:
TELECHONNICATION INFORMATION:
TELECHON ESC 10 487-5800
TELECHONE: 201 343-1684
FELEX: 133521
; INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 18 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-475-055-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFAWQRAMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                             CITY: Hac
STATE: Ne
COUNTRY:
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US-07-755-161A-3
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LOCATION: 2

LIBENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 19"
FRATURE: NFORMATION: thiol group of Cys residue at location 19"
NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 19
OTHER INFORMATION: Oys residue at location 19 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
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APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NASCHIMA, HIDEKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANASKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIARI
TITLE OF INVENTION: VIRAL INPECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57; DB 1; Length 20;
Pred. No. 0.0017;
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COUNTR:
COUNTR:
COUNTR:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
CURRENT APPLICATION DATA:
FILING DATE: O2-MAR-1994
CLASSIFICATION: 514
ATTCANEY/AGENT INPORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DCCKET NUMBER: FUN-019
TELECHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCUMENT NUMBER: FILING DATE:
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VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-204-487-1
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                                            Gaps
      Best Local Similarity 83.3%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 2; Indels
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PRICEL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.

ZIP: 20005
ZORPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: DisplayWrite
COMPUTER: DisplayWrite
COMPUTER: DisplayWrite
COMPUTER: DisplayWrite
CORPUMARE: DisplayWrite
CORPUMARE: DisplayWrite
CORPUMARE: DisplayWrite
TILING DATE: 29-MAY-1992
CLESTICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRAION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 31,367
REFERENCE
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FEATURE:
NAME/KEY: modified site
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL LIVE:
CRLL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
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CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                  1 CFAWORAMRKVR 12
                                                                                                                                                                2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                               RESULT 6
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NAME/KEY:
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US-08-381-984-24
    US-08-256-771-24
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Sequence 24, Application US/08256771

Partent No. 5656591

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING TITLE OF INVENTION: PRODUCTS THEREWITH

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        å
                                                                                                                                                                                                                                                                                                            Query Match 83.8%; Score 57; DB 1; Length 20; Best Local Similarity 83.3%; Pred. No. 0.0017; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                  STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM COMPATIBLE
OFBRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: JULY 22, 1994
PRIOR APPLICATION 1514
PRIOR APPLICATION UMBER:
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                            LENGTH: 20 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                               1 CFAWORAMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 80
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                                         Gaps
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                                                                                                                                                                       RESULT 9
US-08-256-771-25
US-08-256-771-25
Sequence 25, Application US/08256771
Sequence 25, Application US/08256771
GENERAL INFORMATION
APPLICANT: Mamoru TOWITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                         .;
0
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                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKST NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                               1 CFAWQRAMRKVR 12
                                                                                                                 2 CFQWQRNMRKVR 13
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STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
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RESULT 12
US-09-508-734-4

i Sequence 4, Application US/09508734

i Satuence 4, Application US/09508734

i Patent No. 6423509

i GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Wseful microorganism thereof

TITLE OF INVENTION: US/09/508,734

CURRENT PILING DATE: 2000-06-01

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment ther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 0.0017;
0; Mismatches 2; Indels
                                          STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IDEM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CIASIFICATION 1252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER:
  STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGIESTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25:
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INFORMATION FOR SEQ ID NO: 2'SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 83.3
Watches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
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NAME/KEY:
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IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as

OTHER INFORMATION: peptides including the specified peptide as a fragment thered
US-08-381-984-24
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.8%; Score 57; DB 1; Length 20;
83.3%; Pred. No. 0.0017;
live 0; Mismatches 2; Indels
                                                                                                                                                                                AUKRESEE: WEIGHTOLIN, LILLY & FULLES, STREET: 805 Fifteenth Street, N.W., #700 STARET: BO.C. COUNTRY: U.S.A. COMPUTER: D.C. COUNTRY: U.S.A. COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM COMPALIBLE OF STERM: MS-DOS SOFTWARE: WORDSPITCE: S.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/381,984 FILING DATE: APPLICATION NUMBER: US/08/381,984 FILING DATE: APPLICATION NUMBER: TRIENG PATE: ATTORNEY AGENT INFORMATION: NAME: WARTEN N. Cheek, Jr. REGISTRATION WUMBER: 33,367 REFERENCE/DOCKET NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICATE: Manoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
COUMBER OF SEQUENCES:
COMPRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24:
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.33
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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FRAURE:

NAME/KEY: modified site

LOCATION: 4

IDENTIFICATION METHOD:

OTHER INFORMATION: Cys residue at location 21"

FRAURE:

NAME/KEY:

NAME/KEY:

OTHER INFORMATION: Choice "thiol group of cys residue at location 21"

FRAURE:

NAME/KEY:

NAME/KEY:

NAME/KEY:

NAME/KEY:

OTHER INFORMATION: Cys residue at location 21"

IDENTIFICATION METHOD:

OTHER INFORMATION: Cys residue at location 21

OTHER INFORMATION: Cys residue at location 21

OTHER INFORMATION: thiol group of Cys residue at location 4"

AUTHORS:

AUTHORS:

AUTHORS:

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83.8%; Score 57; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 2; Indels
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FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10
    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECHMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEC ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TYPE: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MARP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFAWQRAMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
CELL LINE:
IMMEDIATE SOURCE:
LIBBARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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US-09-508-734-6

US-09-508-734-6

Sequence 6, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and

TITLE OF INVENTION: Useful microorganism thereof

FILE REPERENCE: PA/SC/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT APPLICATION NUMBER: US/09/508,734

PRIOR PILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR PLING DATE: 1998-07-13

SOFTWARE: KOPATENTIN NOWSER: KR1998-29351

NUMBER OF SEQ ID NOS: 12

SOFTWARE: KOPATENTIN 1.71
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Pred. No. 0.002;
                                                                                                                                                                                                                ch 83.8%; Score 57; DB 4; Length 22; l Similarity 83.3%; Pred. No. 0.0019; l0; Conservative 0; Mismatches 2; Indels
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US-70-755-161A-10
US-70-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS: 10
COUNTRY: Washington
STREE: D.C.
COUNTRY: U.S.A.
STREET D.C.
COUNTRY: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910055
TARENT APPLICATION DATA:
TABLESS OF TAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.8%;
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Best Local Similarity 83.3
Matches 10; Conservative
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LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            1 CFAWORAMRKVR 12
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                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                   US-09-508-734-4
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RESULT 15

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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" AUTHORS: AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 1; Length 25;
Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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                                                                                                                                     TITES:
JOURNAL:
VOLUME:
SISSUE:
PAGES:
DOCUMENT NUMBER:
FILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                         83.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFAWQRAMRKVR 12
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Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
                                            Sequence 10, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS: ADDRESSE: Wenderoth, Lind & Ponack
TREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PG-LC.
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 53
PRIOR APPLICATION DATA:
APPLICATION NAMER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNE: WALTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 31,367
REGISTRATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: AMINO acid
TYPE: AMINO acid
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LOCATION: 4
LDCATION: 4
LDENTIFICATION METHOD:
OTHER INFORMATION: Cys
OTHER INFORMATION: thi
FEATURE:
NAME/KEY: modified sit
LOCATION: 21
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
CREANELLE:
IMMEDIATE SOURCE:
LIBRARY:
LIBRARY:
CLONE:
CLONE:
CHROMOSOME/SEGMENT:
MAP POSITION:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
HYPOTHETICAL:
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us-09-743-107b-95.rapb

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APPLICANT: (YSTEIN REKDAL APPLICANT: BALDUR SVEINBJ(RNSSON
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Sequence 2, Appl
Sequence 2, Appli
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                                                                                                                                    February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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Sequence 7, 7
Sequence 8, 7
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Sequence 30,
Sequence 14,
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/ cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep: -
/ cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep: -
/ cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep: -
/ cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep: -
/ cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep: -
/ cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep: -
/ cgn2 6/ptodata/2/pubpaa/USO9 NEW PUB.pep: -
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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todata/2/pubpaa/PCT_NEW_PUB
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US-09-995-542-10
US-09-738-626-4884
US-10-080-960-11
US-09-948-078-2
US-09-988-320-2
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US-10-023-096-2
US-09-798-869-3
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US-09-798-869-4
US-09-798-869-4
US-09-798-869-7
US-09-798-869-7
US-09-798-869-7
US-09-798-869-7
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US-09-798-869-7
US-09-798-869-7
US-09-798-869-10
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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68
1 CFAWQRAMRKVR 12
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                     Sequence:
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Sequence 35744, A Sequence 17, Appl Sequence 19, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 16, Appl Sequence 11, Appl Sequence 10, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl Sequence 1487, Appl Sequence 11887, Appl Sequence 11887, Appl Sequence 11887, Appl Sequence 1118, Appl Sequence 2, Appli Sequence 2, Appli			gth 15; Indels 0; Gaps 0;		
US-09-864-761-35744 US-09-804-56-8 US-09-904-536-8 US-09-904-536-11 US-09-904-536-12 US-09-904-536-13 US-09-904-536-14 US-09-904-536-14 US-09-904-536-14 US-09-904-536-14 US-09-904-536-17 US-09-904-536-17 US-09-904-536-18 US-09-904-536-11 US-09-904-536-11 US-09-983-806-6 US-09-984-886-1119 US-09-764-886-1119 US-09-764-886-11116	ALIGNMENTS	1171 1171 NDSEN (RNSSON 11VE PEPTIDES 10SA-A 10SA-A 10S/09/798,869 0.2-27 0.2-27 0.2-27 131 131 131 139 139 139 139 139	Score 57; DB 9; Length Pred. No. 0.00055; 0; Mismatches 2; Ind		98869 N
46 10 20 20 20 20 20 20 20 20 20 20 20 20 20		n US/0975 0 SVENDSIE EXDAL (RNN AND AND AND AND AND AND AND AND AND A	83.8%; 83.3%; ative	C1 4	ton US/097 80022821A1 RD SVENDSE REKDAL
00000000000000000000000000000000000000		NEGOUTE 1.  Sequence 2. Application US/0979886; Publication No. US20030022821A1 GENERAL INFORMATION: APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: (YSTEIN REKDAL APPLICANT: LARS VORLAND APPLICANT: LARS VORLAND TILLE OF INVENTION: BIOACTIVE PEP FILE REFERENCE: A34049-FCT-USA-A CURRENT PEPLICATION NUMBER: US/09 CURRENT FILING DATE: 1999-08-31 PRIOR FILING DATE: 1998-08-8 SEQ ID NO 2. LENGTH: 15 TYPE: PRI VYPE: PRI VYPE: PRI ORGANISM: HOMO SAPIENS	Similarity 0; Conserva	CFAWORAMRKVR 12 	Applicati To US2003 AATION: HN SIGUR YSTEIN F
๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚๚ ๓๓๓๓๓๓๓๓๓๓๓๓		8-869-2 AE ALTORNA ALT	1 1 Ch		-869-20 se 20, P ttion No INFORM
	E ##	Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 2 APPLICANT BRIOR APP PRIOR FILE PRIOR FILE PRIOR APP PRIOR FILE PRIOR APP APPLICANT SEQ ID NO LENGTH: LENGTH: LENGTH: CRACHIS US-09-798-86	Query Mai Best Loci Matches	20y 1 10b 3	RESULT 2 US-09-798-869-20 ; Sequence 20, R ; Publication NG ; GENERAL INFORM ; APPLICANT: J ; APPLICANT: J
		AC.			

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Gaps
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US-09-798-869-6
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Score 57; DB 9; Length 694;
Pred. No. 0.027;
0; Mismatches 2; Indels
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Pred. No. 0.029;
                                                                                                                                                                                                                                                                                 Generate 6, Application US/09798869
| Publication No. US20030022821A1
| GENERAL INFORMATION:
| APPLICANT: JOHN SIGURD SVENDEN
| APPLICANT: BALDUR SVEINBAN
| APPLICANT: BALDUR SVEINBAN
| APPLICANT: BALDUR SVEINBAN
| APPLICANT: BALDUR SVEINBAN
| TITLE OF INVENTION: BLOACTIVE PEPTIDES
| TITLE OF INVENTION: BLOACTIVE PEPTIDES
| CURRENT APPLICATION NUMBER: US/09/798,869
| CURRENT FILING DATE: 1999-08-31
| PRIOR APPLICATION NUMBER: PCT/GB99/02851
| PRIOR APPLICATION NUMBER: B8818938.4
| PRIOR APPLICATION NUMBER: GB9818938.4
| PRIOR PILING DATE: 1999-08-31
| PRIOR PILING DATE: 1998-08-31
| PRIOR PILING DATE: 1998-08-31
| PRIOR PILING DATE: 1998-08-38
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: PRAESEQ for Windows Version 4.0
| SERIOTH: 15
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: USTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
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SOFTWARE FRAISEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
  83.8%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
Matches 9; Conservative
                                                          10; Conservative
                                                                                                           1 CFAWORAMRKVR 12
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     Query Match
Best Local Similarity
Matches 10; Conserv
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APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz
APPLICANT: Rirecki, Tomasz
APPLICANT: Ogolnick, Paul D.
APPLICANT: Ogolnick, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 83.8%; Score 57; DB 9; Length 25; Best Local Similarity 83.3%; Pred. No. 0.00093; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CIIY: Washington D.C.
COUNTRY: U.S.A.
                           TITLE OF INVENTION: BICACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/799,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FREESEQ for Windows Version 4.0
LENGTH: 25
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REGISTRATION NUMBER: 31,409
REPERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 28EQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CFOWORNMRKVR 14
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Gaps ö

2; Indels

Mismatches

7; Conservative

Matches

g ò

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PEATURE:
OTHER INFORMATION: synthetic peptide (modified form of homo sapiens;
OTHER INFORMATION: sequence)
US-09-798-869-7
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Pred. No. 0.69;
2; Mismatches 3; Indels
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Pred. No. 0.35;
0; Mismatches
                                                                                           GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BLOACTIVE PEPTIDES
FILE REFRENCE: AJ404PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows PERSION 4.0
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ASIGNMENT ASSON APPLICANT: LARS VORLAND TILLS OF INVENTION: BIOACTIVE PEPTIDES TILLS OF INVENTION: BIOACTIVE PEPTIDES FILE REFERENCE: A34049-PCT-USA-A CURRENT FILING DATE: 2001-02-27 CURRENT FILING DATE: 1099-06-31 PRIOR PILICATION NUMBER: PCT/GR99/02851 PRIOR PILING DATE: 1999-08-31 PRIOR APPLICATION NUMBER: PCT/GR99/02851 PRIOR FILING DATE: 1999-08-28 NUMBER: OF SEQ ID NOS: 30 SOFTWARE: PRACER PRIOR DATE: 1998-08-28 SEQ ID NO 7 LENGTH: 15
                                     Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTRIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 63.0.
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US-09-798-869-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%; Score 42; DB 9, 63.6%; Pred. No. 0.21; iive 0; Mismatches
                                                                                                                                                                                                           APPLICANT: (YSTEIN BYENDEN
APPLICANT: (YSTEIN REKOL
APPLICANT: (YSTEIN REKOL
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BLOACTIVE PEPTIDES
TITLE FERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastsEQ for Windows Version 4.0
SEGO ID NO: 23
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PREUSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09798869
Publication No. US2003002281A1
RENEAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTERN REKDAL
APPLICANT: HALDUR SVEINBJ (RNSSON)
APPLICANT: LARS VORLAND
                                                                                                                                                Sequence 23, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.5-
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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                                       3 CYQWORRWRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CYQWQRRMRKL 13
1 CFAWQRAMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: MURINE
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Gaps

3 CLRWONEMRKV 13

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVETINBJ (RNSSON
APPLICANT: LARS VORLAND
ITTLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-U3A-A
FILE REFERENCE: A34049-PCT-U3A-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-09-31
PRIOR PILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-34
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRRESEQ FOR WINGOWS VERSION 4.0
Application US/09798869
No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFAWQRAMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine)
OTHER INFORMATION: sequence)
US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 9; Length 15;
Pred. No. 0.69;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 3
Pred. No. 0.69;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CYCTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYBINBJ RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: 18/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FESSEER FOR WINGOWS VETSION 4.0
SSOFTWARE: PSSEER FOR WINGOWS VETSION 4.0
SSOFTWARE: LES
                                                                                                                APPLICANT: UNEXPENDED
APPLICANT: USETEIN REXDAL
APPLICANT: (YSTEIN REXDAL
APPLICANT: BALDUR SVETNBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                       Sequence 8, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.4%;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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; ORGANISM: BOVINE
US-09-798-869-29
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Length 15; 3; Indels

Score 39; DB Pred, No. 0.69 2; Mismatches

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APPLICANT: Yusupova, Guinara ZH
APPLICANT: Baucom, Albion
APPLICANT: Baucom, Albion
APPLICANT: Baucom, Albion
APPLICANT: Baucom, Albion
APPLICANT: Baucameter, feura
APPLICANT: Dallas, Anne
TITLE OF INVENTION: X-RAY CRYSTAL STRUCTURES OF FUNCTIONAL
TITLE OF INVENTION: AND MODEL MESSENGER RNAS
TITLE OF INVENTION: AND MODEL MESSENGER RNAS
TITLE OF INVENTION: AND MODEL MESSENGER RNAS
TITLE OF INVENTION: AND MODEL WESSENGER RNAS
TITLE OF INVENTION: AND MODEL WESSENGER RNAS
TITLE OF INVENTION: AND MODEL WESSENGER RNAS
TITLE OF INVENTION: ONDER: US 60/254,603
PRIOR FILING DATE: 2000-12-09
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FREEESQ for Windows Version 4.0
SEQ ID NO 14
SEQ ID NO 14
SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
Sequence 14, Application US/10013379
Publication No. 425020188108A1
GRNERAL INFORMATION:
APPLICANT: The Regents of the University of California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: 508 ribosomal protein L16; OTHER INFORMATION: 19iyP US-10-013-379-14
                                                                                                       Cate, Jamie H.
No. US20020188108Aller, Harry F.
Yusupov, Marat M.
Yusupova, Guinara ZH
Baucom, Albion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Thermus thermophilus
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Matches 7; Conserva
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2 FAWQRAMRKV 11

CFRWOWRMKKL 13

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RESULT 12 US-09-798-869-30

|||:|| || 115 FAWRRAYMKV 124

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0; Gaps

Query Match

54.4%; Score 37; DB 10; Length 2310;

Best Local Similarity 75.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 0; Mismatches 2; Indels (

Search completed: February 21, 2003, 08:11:58
Job time : 7.88372 secs

779 CFAWQDRM 786

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1 CFAWQRAM 8

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5.1.3	Compugen
version	- 2003
nCore	1993
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:48:01; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec

US-09-743-107B-95 68 1 CPAWQRAMRKVR 12 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database :

2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	lactotransferrin p	lactoferrin - goat	lactoferrin - shee	ADP, ATP carrier pr	hypothetical prote	lactoferrin precur	carcinoembryonic a	cell cycle arrest	hypothetical prote	phytochrome C - so	33.3K hypothetical	methyl-accepting c	NTP pyrophosphohyd	hypothetical prote	pyridoxamine 5'-ph	pyridoxamine 5'-ph	probable pyridoxam	interleukin-2 rece	interleukin-2 rece	probable dTDP-4-de	gene 20 protein -	hypothetical prote	Deinococcus radiod	membrane lipoprote	probable carbohydr	aDP, ATP carrier pr	hypothetical prote		
SUMMARIES	ID	TEHUL	JC2323	S52107	G71633	AH3147	A28438	D33876	A39654	AB0858	T14803	G86403	E82395	AC3242	C71306	H97451	AB2670	AG3441	JC1113	S07442	T00104	WZBEM6	C33374	B97374	AH2591	F83199	B97842	T01179	C84325	JE0238
	80	-	0	N	N	N																								
	Query Match Length DB	711	708	33	200	121	707	114	306	511	1135	289	561	161	202	206	206	208	275	275	294	303	303	337	337	494	499	502	584	601
ф	Query	3	σ	4	3	61.8	н	œ		~		55.9	w		4		4	4,	54.4	54.4	54.4	4	4	4,	54.4	54.4	4		54.4	54.4
	Score	57	47	44	43	42	42	40	40	39	39	38	38	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
	Result No.	п	71	٣	4	ß	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

hemolysin-type cal protein F21H11.2 [	dynein beta heavy probable membrane	threonine synthase	hypothetical prote hypothetical prote	ы	late 100K protein	valine-tRNA ligase	receptor tyrosine	C. elegans protein	hypothetical prote	conserved hypothet	probable phycocyan	hypothetical prote
B82736 D88450	T08030	E90238	C86624 H72000	C81357	WMAD15	B71250	T31329	D59433	D83181	AB0438	S25308	T22597
01 01	010	N	<b>(1)</b>	(7)	н	N	7	N	7	N	N	~
1636	4568 278	396	4 6 7 6 7	541	807	926	1081	1165	1746	228	243	275
54.4 4.4	54.4	52.9	0.0	52.9	52.9	52.9	52.9	52.9	52.9	51.5	51.5	51.5
37	37.37	,	9 9	36	36	36	36	36	36	35	35	35
				. ~	_	_	_	41	42	_		

## ALIGNMENTS

Н	
ESULT	FHOL

lactotransferrin precursor (validated) - human

C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000 C;Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S7

Alrede to the EMBL Data Library, March 1994
Alreference number: G06820
Alredesabon: G01394
Alredesabon: G01394
Alredesabon: G01394
Alredesabon: G01394
Alredevels preliminary; translated from GB/EMBL/DDBJ
Alredevels L711 - CHO>
Alredevels: L711 - CHO>
Alredevels: L711 - CHO>
Alredevels: Effect Confest MBL: U07643; NID: g467236; PIDN:AAB60324.1; PID: g467237
Alredevels: Maloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
Alritle: Complete nucleotide sequence of human mammary gland lactoferrin.
Alredevent number: S11228; MUID: 90384839; PMID: 2402455
Alredevels: MID: 24024455

A; Molecule type: mRNA
A; Residuce: 1-148, T', 150-422, 'C', 424-711 <REY>
A; Residuce: 1-148, T', 150-422, 'C', 424-711 <REY>
A; Crosa-references: EMBL:X53961; NID: 934415; PIDN: CAA37914.1; PID: 934416
A; Crosa-references: EMBL:X53961; NID: 934415; Panella, T.
R; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Emborrinol. 6, 1959-1981, 1992
Mol. Emborrinol. 6, 1959-1981, 1992
A; Reference number: A45401; MUID: 93125571; PMID: 1480183

Accession: A45401

A Molecule type: DNA
A, Residues: 1-15 < TEN>
A, Residues: 1-15 < TEN>
A, Residues: 1-15 < TEN>
A, Experimences: GBS-52659; NID:g263311; PIDN:AAB24877.1; PID:g263312
A, Experimental source: placenta
A, Mote: sequence extracted from NCBI backbone (NCBIP:122202)
B, Powell, M.J.; Ogden, J.E.
Nucleic Acids Res. 18, 4013, 1990
A, Title: Nucleotide sequence of human lactoferrin cDNA.
A, Reference number: S10324; MUID:90326549; PMID:2374734

Accession: S10324 Molecule type: mRNA Residues: 3-711 <POW>

Status: nucleic acid sequence not shown; not compared with conceptual translation jGross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412; Stcowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W. iochem. J. 276, 349-355, 1991; Jicchem. J. 276, 349-355, 1991; Jittle: Expression of cloned human lactoferrin in baby-hamster kidney cells.; Reference number: S15853; MUID:91264786; PMID:2049066

Molecule type: mRNA Residues: 20-31 <ST1>

A, Molecule type: protein A, Residues: 20-28, 'X', 30-31 <ST2>

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Reduces: 1-500 cAND: A;Reduces: 1-500 cAND: A;Reduces: 1-500 cAND: A;Reduces: 1-500 cAND: A;Reduces: 200 cAND: A;Reduces: 200 cAND: A;Reduces: 200 cAND: CAND
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hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupont hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens
C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AH3147
C;Accession: AH3147
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cipate: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997 Cipates 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997 Cipacession: S23107 #text_change 05-Dec-1997 #text_change 05-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: G71633
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazakii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: G71633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP,ATP carrier protein (11c5) RP739 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lactoferrin - sheep (fragment)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                Length 708
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A Molecule type: protein
A Residues: 1-33 < QTA>
C Superfamily: transferrin; transferrin repeat homology
C Keywords: duplication
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Pred. No. 0.28;
3; Mismatches
                                                      Score 47; DB;
Pred. No. 1.5;
2; Mismatches
                                                Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative 2
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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482 CFAWIYAVRKI 492
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A; Residues: 436-487, 'A', 489-711 <RAD>
A; Residues: 436-487, 'A', 489-711 <RAD>
A; Cross-references: RNBL-M18642; NID:9186815; PIDN:AAA86665.1; PID:9386855
R; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A; Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 3-701, SWKPVN' <PAN>
A; Residues: 3-701, SWFVN' <PAN>
A; Experimental source: normal breast tissue
R; Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Eur. J. Biochem. 145, 659-666, 1984
Eur. J. Biochem. 145, 659-666, 1984
A; Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A; Reference number: A31000; MUID:85076667; PMID:6510420
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C,Superfamily: transferrin, transferrin repeat homology
C,Keywords: duplication; glycoprotein; iron binding; milk
C,Keywords: duplication; glycoprotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-71/Product: lactoriansferrin status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRH2>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;360-63,39-66,135-218,177-183,190-201, 221-266,503-699/595-609/Disulfide bonds: #status errors and site: carbohydrate (Aan) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Recession: S07160
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A,Residues: 1-708 <LEP>
C;Superfamily: transferrin; transferrin repeat homology
C;Kywords: duplication; glycoprotein
F;359-656/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
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R,Le Provost, F: Nocart, M.; Guerin, G.; Martin, P.
R,Le Provost, F: Nocart, M.; Guerin, G.; Martin, P.
Biochem: Biophys Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin GDNA: A;Reference number: JC2323; MUID:94380047; PMID:8093048
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
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Cross-references: GDB:119368; OMIM:150210
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Best Local Similarity
Matches 10; Conserva
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A;Reference number: A33876; MUD:89214106; PMID:2708349
A;Accession: D38876
A;Status: preliminary
A;Molecule type: DNA
A;Redidues: 1-114 <KDNA
A;Cross-references: GB:MG026; NID:g203407; PIDN:AAA40911.1; PID:g554427; GB:J04626; C
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term
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12;
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Pred. No. 4.8;
2; Mismatches
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A;Cross-references: SGD:S0004659; MIPS:YMR055c
A;Map position: 13R
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                                                                                                                                                                                                                                                                                                                                      58.8%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Les 6, Conservative
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A;Accession: S54555
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A,Molecule type: DNA
A,Residues: 1-306 <HOY>
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Best Local S
Matches 6
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R;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
Affitle: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre A;Reference number: A92596; MUID:87280033; PMID:3611056
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cardinoembryonic antigen homolog 4 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jul-1999
C;Accession: D18376
R;Kodelja, V.; Lucas, K.; Barnert, S.; von Kleist, S.; Thompson, J.A.; Zimmermann, W. J. Biol. Chem. 264, 6906-6912, 1989
A;Title: Identification of a carcinoembryonic antigen gene family in the rat. Analysis
                                                                                                                              ster, E.W.
Ayîtıle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Reference number: AB2577; PMID:11743193
A.Accession: AH3147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu, Y.; Teng, C.T.
Biol. Chem. 266, 21880-21885, 1991
Fitle: Characterization of estrogen-responsive mouse lactoferrin promoter.
Freference number: A41205; MUD:92042099; PMID:1939212
A6068810n: A41205
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C'Species: Mus musculus (house mouse)
C'Date: 10-8ep-1999 #sequence_revision 10-8ep-1999 #text_change 10-8ep-1999
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72.07.07/Product: lactotransferrin #status predicted <MAT>
Fi358-695/Domain: transferrin repeat homology <TRH2>
Fi368-695/Domain: cransferrin repeat homology <TRH2>
Fi494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Superfamily: transferrin, transferrin repeat homology
Keywords: duplication; glycoprotein
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Pred. No. 2
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es 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-121 <KUR>
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Residues: 3-707 <PEN>
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A;Residues: 1-15 <LIU>
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Best Local S
Matches 7
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Matches
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hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar hypothetical protein strange albap, enterica serovar Typhi A;Noter this species has also been called Salmonella typhi c;Date: 09-Nov-2001 #text_change 09-Nov-2001 #text_change 09-Nov-2001 #fext_change 09-Nov-20
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A;Residues: 1-306 <DEV>
A;Cross-references: EMBL:Z49703; NID:g817880; PIDN:CAA89765.1; PID:g817888; GSPDB:GN00
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N;Alternate names: protein YM9796.08c; protein YMR055c
C;Species: Sacciaromyces cerevisiae
C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 21-Jul-2000
C;Accession: A39654; S54555; S19034
R;Hoyt, M.A.; Totis, L.; Roberts, B.T.
Cell 66, S07-517, 1991
A;Rtle: Saccharomyces cerevisiae genes required for cell cycle arrest in relaterence number: A39654; WUID:91330299; PMID:1651171
                                                                                                                                             Gaps
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Length 114;
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methyl-accepting chemotaxis protein VCA0974 [imported] - Vibrio cholerae (strain N169. C;Species: Vibrio cholerae (strain N169. C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: B82395 B;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.Opardeon, D.; Ermolaava, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I. R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUD:20406833; PMID:10952301
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C;Genetics:
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A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-161
A;Coss-references: GB:AE008690; PIDN:AAL46353.1; PID:g17744142; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
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hypothetical protein TP0594 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                  CFTWEEYARHVR 19
   CFAWQRAMRKVR 12
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A;Molecule type: DNA
A;Residues: 1-561 <HEI>
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51 AWEAALREVR 60
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A;Genome: plasmid
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., J.; Jin, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.; Sun, H.; Tallon, A;Reference and analysis of Chromosome 1 of the plant Arabidopsis.
A;Retus: preliminary
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C;Species: Sorghum bicolor (sorghum)
C;Species: Sorghum bicolor (sorghum)
C;Accession: TH4803
R;Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet, submitted to the EMBL Data Library, April 1996
A;Reference number: Z18186
A;Recession: T14803
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Relatus: preliminary; translated from GB/EMBL/DDBJ
A;Relatus: preliminary; NID:g1800218; PID:g1800219
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C;Keywords: chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regulat
F;65-581/Domain: phytochrome homology <PHY>
F;321/Binding site: phytochromobilin (Cys) (covalent) #status predicted
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A,Residues: 1-511 <PAR>
A,FOSS-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176
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A;Cross-references: GB:AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141
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3;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 05-Nov-1999

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'Strater, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDchey, L.; Weidam, J.; Smith, H.O.; Venter, J.C.
science 281, 375-388, 1998
'YTitle: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
'Reference number: A71250; MUID:98332770; FMID:965876
'Status: preliminary; nucleic acid sequence not shown; translation not shown
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pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (str C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002

Accession: H97451 'Accession: H97451 'Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, Goodner, B.; Hinkle, G.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; cience 294, 2323-2328, 2001 fittle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum; Reference number: A97359; PMID:11743194

Accession: H97451

Status: preliminary Nolecule Cype: DNA KBeidues: 1-206 «KUR» Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169

A;Gene: AGR C 1381 A;Map position: circular chromosome C;Superfamily: pyridoxamine-phosphate oxidase

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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Nhan W., Parrell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

Gnoj L., la Bastide W., Kaplan N., Greco T., Touchman J., Muzny D.,

Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,

Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,

Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,

Sagripanti J.L.;

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
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Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
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MEDLINE-88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987).
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Haridas M., Anderson B.F., Baker B.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jolles P.;
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              TISSUE-Mammary gland;
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"Nucleotide sequence of human lactoferrin cDNA.";
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MEDLINE=82262043; PubMed=7049727;
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**Rintwoeth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,

**Rintwoeth G.K., Sommer J.R., Basti S., Reddy M.K., Kanai A., Hotta Y.,

**A Sumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,

**A Sumaramanicavel G., Muniar F., Schorderete D.F.,

**B Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakasu K.,

**B I Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakasu K.,

**B I Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakasu K.,

**B I Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakasu K.,

**B I Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakasu K.,

**Pemilial subepithelial corneal amyloidosis (gelatinous drop-like corneal dystrophy): exclusion of linkage to lactoferrin gene.";

**Mol. Vision 4:31-32(1998).

**CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUMALY BICARDANATE.

**PUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST

**CORNEAL MAION A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE FOR MATAGONIST FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Ifo K., Chiba H., Yoshikawa M.;
"Isolation and characterization of oploid antagonist peptides derived from human lactoferrin.";
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
\Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                        Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N., Structures of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: MONOMER.
-i- SUBCELLULAR LOCATION: Secreted.
-i- DOWAIN: COMPOSED OF TWO HOWCLOGGUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                              X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). MEDLINE=99192677; PubMed=10089508;
                                                                                                                                                                                                                                                                                                                                                  Agric. Biol. Chem. 54:1803-1810(1990).
                                                         Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X53961; CAA37914.1; -.
EMBL; U07643; AAB60324.1; -.
EMBL; M93150; AAA36159.1; -.
EMBL; M93205; AAA59511.1; -.
EMBL; M93205; AAA58656.1; -.
EMBL; M18642; AAA86665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF332168; AAG48753.1; -. BC015822; AAH15822.1; -. BC015823; AAH15823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; CAA37116.1; -. ; AAB57795.1; -. TFHUL.
                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS THR-30 AND ARG-48.
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1LCT; 31-OCT-93
                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9873069;
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12-MAR-97. 21-APR-97.

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38 CAQWQRRMKKVR 49
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                                                                                                                                                                                                                                                                                                         708 AA;
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Best Local Similarity
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                              Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (UN1-199) to the EMBL/Genbank/DDBU databases.
-!-FUNCTION: TRANSFERINS ARE IRON BINDING TRANSFORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FEREIC IRON IN ASSOCIATION WITH THE BINDING
-!-SUBUNIT: MONOMER (BY SIMILARITY).
-!-SUBUNIT: MONOMER (BY SIMILARITY).
-!-SUBCELLULAR LOCATION: Secreted.
-!-DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!-SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                             Gaps
                                                                                                                                                                                       Camelus dromedarius (Dromedary) (Arabian camel).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                                                      STRAIN-Somali; TISSUB-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; ITRO1156; Transferrin.
Pfam; PF00405; transferrin; 2.
Pfam; PF00405; transferrin; 2.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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0
      83.8%; Score 57; DB 1; Length 711;
83.3%; Pred. No. 0.0052;
iive 0; Mismatches 2; Indels
                                                                                                                  TRFL_CAMDR STANDARD; PRT; 708 AA. 09TUMO; 09MZSS; 16-007-2001 (Rel. 40, Created) 6-007-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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LACTOTRANSFERRIN.
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EMBL, AF165879; AAF82241.1; -.
HSSP, O77811; 1B1X.
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                 39 CFOWORNMRKVR 50
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005962;
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                                                                                                                                                                InterPro; INTO, Laneferrin.
Pfam; PF004105; transferrin, 2.
PRINTS; PR00405; transferrin, 2.
PRINTS; PR00405; TRANSFRRIN.
SMART; SM00042; TRANSFRRIN.
PROSITE; PS00205; TRANSFRRIN. 1; 2.
PROSITE; PS00205; TRANSFRRIN. 2; 2.
PROSITE; PS00207; TRANSFRRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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L -> R (IN REF. 2).
F -> P (IN REF. 2).
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F -> P (IN REF. 2).
D -> G (IN REF. 2).
P ZEDA3C8339960D CRC64;
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IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC...)
-1- DCMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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77358 MW;
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EMBL; X78902; CAA55517.1; -.
HSSP; O77698; 1CE2.
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708 AA;
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STRAIN=Madrid E;
MEDLINE=99039499, bubMed=9823893;
MEDLINE=29039499.
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
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Pred. No. 1.4;
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InterPro; IPRO04667; ADP_ATP_car.
Pfam; PF03219; TLC; 1.
TIGRERAMS; TIGR00769; AAA; 1.
TIGRERAMS; TIGR00769; AAA; 1.
TIGRERAMS; TIGRO0769; AAA; 1.
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     15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CAY-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein 5 (ADP/ATP translocase 5)
TLCE OR TLC5 OR RP739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 396:133-140(1998).
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu Y., Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885 (1991)
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OP AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pentecost B.T., Teng C.T.; "Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (AFR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Uterus;
Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: SECRETED.
SUBCELLULAR EDELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                              TRFL MOUSE STANDARD; PRI; 707 AA. P08071; P70509; Q922P2; C1-AUG-1988 (Rel. 08, Created) PL-MX-2002 (Rel. 41, Last sequence update) 15-UW-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, J03298, AAA40525.1; --
EMBL, D8810.0, BAA13633.1; --
EMBL, BC006904, AAH06904.1; --
EMBL, M74778, AAA39427.1; --
FIR, A28438, A28438.
MGD, MGI:96837, LLf.
INCEPPO, IPRO01156; Transferrin.
Pfam, PF00405, transferrin.
PRINIS; PR00422: TRANSFERRIN.
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PROSITE; PSO0205; TRANSFERRIN 1; 1.
PROSITE; PSO0206; TRANSFERRIN 2; 2.
PROSITE; PSO0207; TRANSFERRIN 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEDLINE=87280033; PubMed=3611056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-14 FROM N.A.
                         482 CFAWIYAVRKI 492
1 CFAWQRAMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Gaps
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01-AUG-1992 (Rel. 23, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
BUB2 OR YMR055C OR YM9796.08C.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomyceties; Saccharomycetales; Saccharomycetales; Saccharomyceties; NOBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91330299, PubMed=1651171;
Hoyt M.A., Totis L., Roberts B.T.;
S. cerevisiae genes required for cell cycle arrest in response to loss of microtubule function.";
Cell 66:507-517(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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IRON 2 (BY SIMILARITY).
IRON 6 (BY SIMILARITY).
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N-LINKED (GLCNAC. . . )
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MR -> IQG (IN REF. 2
R -> Q (IN REF. 2
M -> L (IN REF. 2
LACTOTRANSFERRIN.
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Matches 7, Conservative
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SEQUENCE FROM N.A.
STRAIN=S288C;
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SEQUENCE FROM N.A.
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ID BUB2_YEA
AC P26448;
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5; Conservative
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P12342;
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Matches
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                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB outstation the butwopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.sib.ch).
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-!- FUNCTION: REGULATORY PHOTORRCEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                    "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
                                                                                                               regulates cytokinesis.";
J. Cell Sci. 114:2345-2354(2001).
-!- FUNCTION: Part of a checkpoint which monitors spindle integrity and prevents premature exit from mitcais. This cell-cycle arrest depends upon inhibition of the G-protein Teml by the BFA1/BUB2
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Childe K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.B.;
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                             MEDLINE-21385309; PubMed=11493673;
Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fesquet D.,
Johnston L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.8%; Score 40; DB 1; Length 306; 60.0%; Pred. No. 3.1; ive 1; Mismatches 3; Indels
STRAIN=S288c / AB972;
Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell cycle, Mitosis.
SEQUENCE 306 AA, 35027 MW; AlDDBFB548E81EA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHYC_SORBI STANDARD; PRT; 1135 AA. P935Z8; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 115-UUN-2002 (Rel. 41, Last annotation update) Phytochrome C.
                                                                                                                                                                                            -!- SUBUNIT: Interacts with BFA1.
-!- SUBCELLULAR LOCATION: Spindle poles.
-!- SIMILARITY: TO S.POMBE CDC16.
                                                                                                                                                                                                                                                                                                                                                    EMBL; M64706; AAA16885.1; -.
EMBL; 249703; CAR89765.1; -.
PIR, A39654; A39654.
SGD; S0004659; BUB2.
InterPro; IPR000195; RabGAP_TBC.
Pfam; PP00566; TBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 CFAWQTQQRR 117
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Matches 6; Conserv
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                                                   CHARACTERIZATION.
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RECOUNTED TO PER CANCERS.

RESPONSES. PR. COUTTOLS THE REPRESSION OF A NUMBER OF NUCLEAR GENES INCOLUDING THOSE RECOINTS.

REPROSTALISON OF PER NOCHMAN. THE SMALL SENIOR TO PER NOCHMAN. THE SMALL SENIOR OF THE SMALL SENIOR OF
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Ovis aries (Sheep).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
      01-AUG-1992 (Rel. 23, Last sequence update)
01-RBB 1-1996 (Rel. 33, Last annotation update)
Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PSS) (TAC antigen) (CD2S).
                                                                                                                                         Verhagen A.A.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                 NCBI_TaxID=9940;
                                                                                                                               rissum=T-cell;
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TRANSMEM
DOMAIN
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                                                 IL2RA.
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                                                                                                                                  MEDLINE-88212503; PubMed=2835311;
MEDLINE-88212503; PubMed=2835311;
Meinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S., Reeves R., Magnuson U.A., Reeves R., Magnuson U.A., "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
Immunology 63:603-610(1988).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.4%; Score 37; DB 1; Length 275; Best Local Similarity 50.0%; Pred. No. 10; Matches 6; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4901BBF9A4862390 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUSHI 1.
SUSHI 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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EMBL; U24226; AAC46487.1; --
PIR; S07442; S07442.
HSSP; P01589; 11LM.
InterPro; IPR004036; Sushi_SCR_CCP.
Pfam; PR00004; sushi; 2.
SMART; SM00032; CCP; 2.
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122
123
153
160
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275 AA;
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TRANSMEM
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DISULFID
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CARBOHYD
SEQUENCE
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                                                                                         protein, CD25.";
Gene 113:283-284(1992).
-- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
-- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
-- SUBUNIT: NON COVALENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW APPINITY MONOMER (ALPHA
CHAIN): THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.
-- SUBCELIULAR LOCATION: Type I membrane protein.
-- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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SEQUENCE FROM N.A.
MEDLINE-92241682; PubMed=1572550;
BUJGOS R., Sargan D.R., Williamson M.L., McConnell I.;
"Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor, Repeat, Signal, Sushi.
BY SIMILARITY.
INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
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SUSHI 1.
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC.
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Pred. No. 10;
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EMBL; X60149; CAA42723.1; -.
EMBL; A19167; CAA01447.1; -.
PIR, S18891; S18910.
PIR, S18899; S18899.
PIR; J01113; JC1113.
HSSP; P01589; IILM.
INTERPO; IRRO00436; Sushi_SCR_CCP.
PEam; PP00084; sushi; 2.
SWART; SM00032; CCP; 2.
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184
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Gaps

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275 AA.

01-AUG-1992 (Rel. 23, Created)

STANDARD;

SHEEP

RESULT 9
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ID IL2A SHE
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Mol. Biol. RVO.1. 13:1141-1150(1996).
Mol. Biol. RVO.2. 13:1141-1150(1996).
ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR BPR FORM THAT PRODUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR IN PRECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Nipponbare, Takano M.; Tahir M., Kanegae H., Takano M.; "Phytochrome C (PHYC) gene in rice: isolation and characterization of a complete coding sequence."; (In) Plant Gene Register PGR98-210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
Rukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae,
Ehrhartoideae; Oryzeae, Oryza.
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MRDLINES-97010962. PubMed-8865668;
Mathews S., Sharrock R.A.;
"The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot andiosperms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.4%; Score 37; DB 1; Length 601; 45.5%; Pred. No. 23;
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WD 10.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                  EMBL, U86011, AAC26321.1; -.
InterPro; IPR001680; WD40.
PEAM; PR00400; WD40; 10.
PRINTS; PR00320; GPROTEINBRPT.
SWART; SW00320; WR040; 10.
PROSITE; PS00678; WD REPEATS 1; FALSE_NEG.
PROSITE; PS50284; WD_REPEATS_2; 6.
PROSITE; PS50284; WD_REPEATS_2; 6.
PROSITE; PS50284; WD_REPEATS_2; 6.
REPEAL; WD_REPEATS_2; 6.
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601 AA;
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"A novel 66-Kba stress protein, p66, associated with the process of cyst formation of Physarum polycephalum is a Physarum homologue of a yeast actin-interacting protein, Alpl.",
J. Blochem. 124:326-331(1998).
-!- FUNCTION: ASSOCIATED WITH PEPROCESS OF CYST FORMATION.
-!- SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: BELONGS TO THE AIP! FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                       MEDLINE=9233368; PubMed=1321287;
Mibroline J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B., Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B., Honess R.W.;
"Primary structure of the herpesvirus saimiri genome.";
J. VIZOI. 66:5047-5058 (1992).
J. VIZOI. 66:5047-5058 (1992).
EHV-1 37, EBU BERRI, HCMV UL76, ILTV ORF3, AND VZV 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
66 KDa stress protein (p66).
Physarum polycephalum (Slime mold).
Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
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Pfam; PF01646; Herpes UL24; I.
SEQUENCE 303 AA; 34942 MM; DF6D59F7A1C83A0B CRC64;
                                                                                                                                                                      Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                     303 AA
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MEDLINE=98351989; PubMed=9685722;
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Matches 6; Conserv
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P90587;
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RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHICADPHYLL, B BIDDING EROTEIN, PROTOCHLOROPHYLLIDE REDUCTAGE, RINA, ETC. IT ALSO CONTROLS.
-!- FHE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
-!- FUMILARITY HOWODIMER (BY SIMILARITY).
-!- FUMILARITY: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOWAIN.
-!- SIMILARITY: CONTAINS 1 HAS-BASSOCIATED C-TERMINAL
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C -> S (IN REF. 2).
MW; F2A520161CFE7832 CRC64;
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INTERPRO; IPRO03594; ATPDING ATPRSSE.
INTERPRO; IPRO036194; ATPDING ATPRSSE.
INTERPRO; IPRO04559; HIS KIN Sig.
INTERPRO; IPRO001619; PAC.
INTERPRO; IPRO00014; PAS. domain.
INTERPRO; IPRO001294; Phytochrome.
PÉGM; PRO0512; Signal; 1.
PÉGM; PRO0512; Signal; 1.
PÉGM; PRO0512; Signal; 1.
PÉGM; PRO0519; PAS; 2.
PÉGM; PRO1590; GAP; 1.
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SNART; SMO005; GAF; 1.
SMART; SM00387; HATPASE c; 1.
SMART; SM00388; HISKA; 1.
SMART; SM00091; PAS; 2.
IIGREAMS; TIGRO0229; SENSORY bo
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EMBL; U61207; AAR41996 1. -
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1137 AA;
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                                                                                           54.4%; Score 37; DB 1; Length 1137; 45.5%; Pred. No. 44;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Potential cation-transporting ATPase (EC 3.6.3.-).
AT5G23630 OR MQM1.11.
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PROSITE; PS00154; ATPASE E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
                Embryophyta; Tracheophyta;
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MEDLINE-20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. X. Se features of the regions of 3,076,755 bp covered by sixty P1 and
                                                                                                                                                                                    Feature. -
clones.";
DNA RES. 7:31-63(2000).
INTERNSPORT OF CATIONS (POTENTIAL).
-!- CATALYTICA CATIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR INCATION: Integral membrane protein.
-!- SUBCELLULAR INCATION: INTEGRAL CATION TRANSPORT ATPASES FAMILY
-!- STAPASES). SUBFAMILY V.
(E1-E2 ATPASES). SUBFAMILY V.
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MAGNESIUM (BY SIMILARITY).
MW; 4A3E82D2222A4D78 CRC64;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core en euroside II; Brassicales; Brassicaceae; Arabidopsis.
Viol_TaxID=3702;
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44.4%; Pred. No. 4
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InterPro; IPR001757; ATPase_E1-E2.
InterPro; IPR01454; HIgnase_/hydxlase.
Pfam; PF00122; B1-E2 ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
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816 816
1179 AA; 131115
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"Retinal stimulates ATP hydrolysis by purified and reconstituted ABCR, the photoreceptor-apecific ATP-binding cassette transporter responsible for Stargardt disease.";
J. Biol. Chem. 274:8269-8281(1999);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97207641; PLDMed=9054934;
Allikmets R., Singh N., Sun H., Shroyer N.F., Hutchinson A.,
Allikmets R., Singh N., Sun H., Shroyer N.F., Hutchinson A.,
Chidambaram A., Gerrard B., Baird L., Stauffer D., Pelifer A.,
Rattner A., Smallwood P.M., Li Y., Anderson K.L., Lewis R.A.,
Nathans J., Leppert M., Dean M., Lupski J.R.,
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mutated in recessive Stargardt macular dystrophy.";
Nat. Genet. 15:236-246(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A., AND VARIANTS STGD TRP-18 AND CYS-212.
MEDLINE=98163759; PubMed=5903029;
Gerber S., Rozet J.-M., van de Pol T.J.R., Hoyng C.B., Munnich A.,
Blankenagel A., Kaplan J., Cremers F.P.M.;
"Complete scon-intron structure of the retina-specific ATP binding
transporter gene (ABCR) allows the identification of novel mutations
underlying Stargardt disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97345663; PubMed=9202155; Azarian S.M., Travis G.H.; Azarian S.M., Travis G.H.; Travis G.H.; Travis G.H.; The photoroceoptor rim protein is an ABC transporter encoded by the gene for recessive Stayardt's disease (ABCR)."; FEBS Lett. 409:247-252(1997).
                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-98141123; PubMed-9490294;
Nagonkin I., Illing M., Koehler M.R., Schmid M., Molday R.S.,
                                                                                                                                   ABCR HUMAN STANDARD; PRT; 2273 AA.
P78353; 060438; 060915; 015112;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Retinal-specific ATP-binding cassette transporter (RIM ABC transporter) (RIM protein) (RMP) (Stargardt disease protein)
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[7]
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                                           1144 CYSWERLLR 1152
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1 CFAWQRAMR 9
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STRAIN=21gr; MEDLINE=94274778; PubMed=8006077; Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy

Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales, Chlamydomonadaceae, Chlamydomonas.

Chlamydomonas reinhardtii.

SEQUENCE FROM N.A. NCBI\_TaxID=3055

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynain beta chain, flagellar outer arm.
ODA4 OR ODA-4 OR SUP1.

STANDARD;

CHLRE

DYHB

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VARIANTS STGD E-60; T-60; E-65; L-68; R-72; C-212; S-230; S-247; V-328; K-471; P-541; Q-572; R-607; K-635; C-653; Y-764; R-765; A-901; I-959; K-1036; V-1038; P-1067; C-1097; C-1108; L-1380; K-1399; P-1430; H-440; H-1443; L-1486; Y-1888; M-1537; P-1689; L-1705; T-1733; R-1748; P-1763; K-1885; H-1898; E-1961; R-1975; S-1977; G-2077; W-2077 AND V-2241, AND VARIANTS Q-152; H-212; R-423; I-552; R-914; Q-943; T-1562; I-1868; M-1921; L-1948; F-1970; A-2059; N-2177 AND
                                                                                                                                                                                                                                                                 "A comprehensive survey of sequence variation in the ABCA4 (ABCR) gene in Stargardt disease and age-related macular degeneration."; Am. J. Hum. Genet. 67:800-813 (2000).
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MEDLINE=20174852; PubMed-10711710;
Simonelli F., Testa F., de Crecchio G., Rinaldi E., Hutchinson A., Atkinson A., Dean M., D'Urso M., Allikmets R.;
"New ABCR mutations and clinical phenotype in Italian patients with Stargardt disease.";
Invest. Ophthalmol. Vis. Sci. 41:892-897(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS STGD ASP-340; GLN-572; ALA-863; SER-965; VAL-1038; ALA-1780
AND HIS-1898, AND VARIANT GLN-943.
MEDLINE=20208356; PubMed=10746567;
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Papaioannou M., Ocaka L., Bessant D., Lois N., Bird A.C., Payne A.,
Bhattacharya S.S.;
"An analysis of ARC mutations in British patients with recessive
retinal dystrophies.";
Invest. Ophthalmol. vis. Sci. 41:16-19(2000).
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MEDLINE-20472331; PubMed-11017087;
Sun H., Smallwood P.M., Nathans J.,
"Blochemical defects in ABCR protein variants associated with human
                                                                                                                                                                           MEDLINE-20442027; PubMed=10958763;
Rivera A., White K., Stoehr H., Steiner K., Hemmrich N., Grimm T.,
Jurklies B., Lorenz B., Scholl H.P.N., Apfelstedt-Sylla E.,
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Eksandh L., Ekstroem U., Abrahamson M., Bauer B., Andreasson S.;
                                                                                                                                                                                                                                                                                                                                                         VARIANTS CORD3 GLU-65; CYS-212; PRO-541; ALA-863; GLY-863 DEL; VAL-1038; LYS-1122; TYR-1490 AND ASP-1598.
MEDLINE-20442040; PubMed=10958761;
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Pred. No. 89;
0; Mismatches 2; Indels
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75.0%;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                  chain genes.";
J. 107:635-644(1994).

J. CELI SCI. 107:635-644(1994).

-!- FUNCTION: PORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.

-!- FUNCTION: PASS A PAST OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GANGA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.

-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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ATP (POTENTIAL).
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Pfam; PF03028; Dynein heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
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Job time : 6.2093 secs
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ALIGNMENTS
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086603
098603
0980HC2
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096251
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09M7A9
08VWN1
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035600
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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Q8TCD2
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Q9tuy5 homo sapien
Q9tu80 ovis aries
Q8ti6k3 agrobacteri
G51104 rattus norv
Q63112 rattus norv
Q63112 rattus norv
Q8462 salmonella
Q87685 lycopersico
Q96602 arabidopsis
Q9604 vibrio chol
Q9604 vibrio chol
Q9byt vibrio chol
Q9kyt homo sapien
Q9kyt homo sapien
Q9kyt homo sapien
Q9byt homo sapien
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(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Q9UCYS
Q9UCK3
Q8U6K3
Q631102
Q8Z462
Q9SW6
Q9SW6
Q9CGN2
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Gapop 10.0 , Gapext 0.5
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sp_plant:*
sp_rodent:*
sp_virus:*
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Q80618 agrobacteri
Q8863 treponema p
Q8863 treponema p
Q8863 treponema p
Q92718 trizobium m
Q87518 brucella me
Q845190 actinobacil
Q9408 actinobacil
Q66251 actinobacil
G66251 actinobacil
G66251 actinobacil
G66251 actinobacil
G8476 pyrobaculum
Q84077 oryzias lat
Q8411 pseudomonas
Q94307 oryzias lat
Q9441 pseudomonas
Q94315 frickettsia
G65237 arabidopsis
Q95415 darabidopsis
Q95417 darabidopsis
Q95617 darabidopsis
Q95617 darabidopsis
Q9781 caenorhabdi
Q87789 oryza sativ
Q87401 triticum ae
Q87789 caenorhabdi
Q87789 caenorhabdi
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29ups0 homo sapien
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
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Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databases.
SEMBL; BC022147; AH22347.1; -
SEQUENCE 711 AA; 78327 WW; 1B9C7EE097C45FAF CRC64;
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Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin I., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Bliber P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;

Nester E.W.;

CSB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaXID=10116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=BD II, TISSUB=LIVER;
MEDLINE=89214106; PubMed=2708349;
Kodelja V., Ludas K., Barnert S., von Kleist S., Thompson J.A.,
Zimmermann W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of a carcinoembryonic antigen gene family in the Analysis of the N-terminal domains reveals immunoglobulin-like, hypervariable regions.";

J. Baol. Chem. 264:6306-6312 (1989),

EMBL; M60026; AAA40911.1; -.

NON TER.

NON TER.
                                                                                                                                                                                                                                                                                                                   61.8%; Score 42; DB 16; Length 121; 63.6%; Pred. No. 4.8; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.8%; Score 40; DB 11; Length 114; Best Local Similarity 60.0%; Pred. No. 10; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                      EMBL; AE009409, AAL45598.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 121 AA; 14085 MW; EBAF41617A3CEA53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 AA; 12832 MW; 3AE108689B061686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Carcinoembryonic antigen-related protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 AA
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Carcinoembryonic antigen (Fragment)
                                                                                                                                                                                                                    Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q63104;
01-NOV-1996 (TrEMBLrel. 01,
01-JAN-1999 (TrEMBLrel. 09,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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42 FAWYRGLRKI 51
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063104
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963112
AC 96311
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNJ-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin (Fragment).
Ovis aries (Sheep).
Exharytota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eucharytos; Coratiodactyla; Ruminantia; Pecora; Bovoidea;
11 TaxID=9940;
                                                                                                                                   "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.13;
0; Mismatches 2; Indels
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Pred. No. 0.56;
3; Mismatches 2; Indels
                                                                                                                                                                                                          InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5B3DDBB CRC64;
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Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Atu4804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AA
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MEDLINE-95127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D.
Biochim. Biophys. Acta 1243:25-32(1995)
usqp. O77698; ICE2.
                                                                                                                                                    seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                                  SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
Sato I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.7%;
54.5%;
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Similarity 81.8%;
9; Conservative (
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Matches 6; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                NCBI_TaxID=9606;
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QBUEK3;
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Q8U6K3
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Q9TR80
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Gaps

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MEDLINE=99413290; PubMed=10485280;
Kerckhoffs L.H., Kelmenson P.M., Schreuder M.E., Kendrick C.I.,
Kendrick R.E., Hanhart C.J., Koornneef M., Pratt L.H.,
Cordonnier-Pratt M.M.,
"Characterization of the gene encoding the apoprotein of phytochrome
B2 in tomato, and identification of molecular lesions in two mutant
                                                                                                                                                                                                                       Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eussterids I; Solanales; Solanaceae; Solanum.
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1121 AA; 125308 MM; ED9EDA704BB37F27 CRC64;
                                                                         (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Last sequence update)
Last annotation update)
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54.5%; Pred. No. 1.6e+02;
iive 1; Mismatches 4.
                 PRT; 1121 AA
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gengory box; 2.
H SHORT; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alleles.";
Mol. Gen. Genet. 261:901-907(1999).
EMBL; AF122901; AAD50631.1; -.
InterPro; IPR002198; ADH short.
ThterPro; IPR003594; ATPbind_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00061; ADH SHORT; UNKNOWN PROSITE; PS000245; PHYTOCHROWE 1; 1. PROSITE; PS50046; PHYTOCHROME 2; 1. SEQUENCE 1121 AA; 125308 WW; ED9
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InterPro; IPR001294; Phytochrome.
Pfam; PF01599; GAP; 1.
Pfam; PF02518; HATPase c; 1.
Pfam; PF00389; PAS; 2.
Pfam; PF00380; phytochrome; 1.
Pfam; PF001213; signal; 1.
PRINTS; PR01033; PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR003661; His kinA.
IPR004359; HIS KIN sig.
IPR001610; PAC.
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SWART; SM00387; HATPARE C; 1.
SMART; SM00388; HisKA; Ī.
SMART; SM00086; PAC; 1.
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             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 54.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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STRAIN=Z17561;
Fallarino A.;
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SMART; SM00086;
SMART; SM00091;
                                                                                                                                                                          Phytochrome B2.
PHYB2.
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                                                                         01-MAY-2000
01-MAY-2000
01-JUN-2002
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InterPro;
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             9SMS60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhi.
Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
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                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN-SPRAGUS-DAWLEY; TISSUE=LIVER;

KMEDLINE-90243655; PubMed=2335509;

REDSTOKE 50. Lucas K., Thompson J.A., Zimmermann W.;

"CONA and gene analyses imply a novel structure for a rat

"Carcinoembryonic antigen-related protein.";

"O. Biol. Chem. 265:7872-7879(1990).

REMEL; M2475; AAA66038.1; -.

RINE-Pro; IPRO03599; IG ...

InterPro; IPRO03069; IG ...

RINE-REMI; PRO047; ig; 2.

RARRT; SMOA409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.8%; Score 40; DB 11; Length 234; 60.0%; Pred. No. 22; 2; Indels 1ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57:4%; Score 39; DB 16; Length 511; 58.3%; Pred. No. 72;
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                                                                                              Rebstock S., Lucas K., Thompson J.A., Zimmermann W.A., Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 AA; 26171 MW; 69BBC9EE0C773F2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:848-852(2001).

EMBL, AL621276; CAD06649.1; -
HYpothetical protein; Complete proteome,
SEQUENCE 511 AA; 58126 NW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                  TRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFAWQRAMRKVR 12
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 FAWYRGLRKI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FAWORAMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
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nes 7; Conser
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NCBI_TaxID=601;
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Q82462; Q82462

RESULT 7 **Q8Z462** 

Query Match

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Gaps

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Indels

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Query Match

Best Loca Matches

ò 엄 RESULT 8 Q9SWS6

SRZ

Q9CGN2; RESULT 10 Q9C6N2

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SEQUENCE FROM N.A.
STRAIRE D. TOK NIGS61 / SEROTYPE 01;
MEDLINE=EL TOK NIGS61 / DEMONDED 1952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Malzberg S.L., Smith H.O., Colwell R.N., Mekalanos J.J., Venter J.C.,
Frager C.M.,
                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabatu S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Phyllobacteriaceae, Mesorhizobium.
NCBI_TaxID=381,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.9%; Score 38; DB 16; Length 329; 60.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein; Complete proteome.
SEQUENCE 329 AA; 34754 MW; 78FC399867F6F3D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61113 MW; DDA599779A000D64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Methyl-accepting chemotaxis protein.
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              561 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                           MEDLINE=21082930; PubMed=11214968;
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InterPro; IPR004090; Me chemotax
InterPro; IPR004090; T. SNARE.
Pfam; PF00672; HAMP; 1.
Pfam; PF00615; MCPsignal; 1.
Pfam; PR00500, CHEMTRNSDUCR.
SMART; SM00283; MA; 1.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP003001; BAB50102.1; -. InterPro; IPR003760; Bmp. Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:477-483(2000).
EMBL; AE004423; AAF96870.1; -.
HSSP; P02942; 1QU7.
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63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                         7:331-338 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 6, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FAWORAMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 FAWEDALKKV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                   STRAIN=MAFF303099;
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Mesorhizobium loti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
SEQUENCE 561 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholerae.
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                                                                                                                                                                                                                                                                                                                                                           DNA Res.
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Q9KKX6;
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STRAIN=CV. COLUMBIA;

WEDLING=219, DubMed=11130712;

Theologis A., Zecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Zecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Chan D., Conway A.B., Conway A.B.,

Buehler E. Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., Dewar K.,

Chung M.K., Con L., Conway A.B., Conway A.B., Frag J.-D., Fong B., Fujii C.Y.,

Chung M.K., Cod H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Inngin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Lin C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Naiti R., Marziali A.,

Lin S., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Milischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Pai G., Peterson J., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

"Herback T., Van Aken S., Vaysberkaia V.S., Walker M.,

"Herback T., Van Aken S., Waysbers R.W.,

"Herback T., Van Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Van Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Van Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Van Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Van Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Van Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Van Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Van Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Wan Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Wan Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Wan Aken S., Waysbers L. C., Davis R.W.,

"Herback T., Wan Aken S., W
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Pred, No. 61;
1; Mismatches 5; Indels
                                                                                                         2; Length 134;
          to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408:816-820(2000).
EMBL; AC079280; AAG50577.1; -.
Hypothetical protein.
SEQUENCE 289 AA; 33338 MW; 753AA27BED0F840C CRC64;
     Submitted (JUL-1998) to the EMBL/GenBank/DDBJ database:
EMBL; AJ231110; CAA13152.1; -.
SEQUENCE 134 AA; 15496 MW;· BF340DBC6554BFAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Hypothetical 33.3 kDa protein.
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   289 AA
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                                                                                                      55.9%; Score 38; DB 63.6%; Pred. No. 28; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                1-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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MLR3148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFAWQRAMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CFTWEEYARHVR 19
                                                                                                                                                                                                        2 FAWORAMRKVR 12
                                                                                                                                                                                                                                                     7 FAWMRALRIKR 17
                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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Q98GW4;
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Matches

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RESULT 11

098GW4 1D 009 AC 009 DT 001 DT 001 DT 001 ON MI

Gabs

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PRT; 1417 AA

560 AWKRAVRGVR 569

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Gaps

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3; Indels

1; Mismatches

Conservative

7;

Matches

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PRELIMINARY;
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                                                                          Q9NYF4
                               RESULT 15
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Prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:65-73(2000).
EMBL; AB037801; BAA92618.1;
Interpro, IPR003347; TF JmjC.
Pfam; PF02273; jmjC; 1.
                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIAA1380 protein (Fragment).
KIAA1380 protein (Fragment).
KIAA1380.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Straubberg'R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001202; AAH01202.1; -.
Interpro; IPR003347; TF_JmjC.
Pfam; PF02273; JmjC; 1.
Hypothetical protein.
SEQUENCE 759 AA; 84712 MW; SAI3F19C0EE952EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER 1 1
SEQUENCE 1265 AA; 141291 MW; 33DB5BE53A7D9EBE CRC64;
                                                                                                                                                                                                (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCT-2000 (TrEMBLrel. 15, Created)
L-OCT-2000 (TrEMBLrel. 15, Last sequence update)
L-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.9%; Score 38; DB 4; I
70.0%; Pred. No. 1.6e+02;
tive 2; Mismatches 1;
                                                                                                                                                            759 AA
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                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                      Hypothetical 84.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.0
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                           fomo sapiens (Human)
2 FAWORAMRKVR 12
                                        7 PAWMRALRIKR 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:||:||
17 AWKRAVRGVR 26
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Q9BVH6;
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01-JUN-2002 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                Putative zinc finger protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Crordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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EMBL, AF251039, AAF63765.1; -
InterProx; IFR003347; FF_JmjC.

Pfam; PF02373; JmjC; 1.

SEQUENCE 1417 AA; 154720 MW; E9CF503D8654FD2B CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Best Local Similarity 70.00,
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TISSUE=BONE MARROW
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                                                                                                                                             Pebruary 21, 2003, 07:37:21 ; Search time 28.093 Seconds
(without alignments)
56.918 Million cell updates/sec
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GenCore version 5.1.3.
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AAY78080
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Gapop 10.0 , Gapext 0.5
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1 CFQLKKNMKKVR 12
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Maximum DB seq length: 2000000000
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## ALIGNMENTS

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Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis; Candida infection; fungicidal, bactericidal, preservative.
                                                                             Human lactoferrin derived peptide SEQ ID NO:96.
                  AAY78096 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                        98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                           (first entry)
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                                                                                                                                                                               WO200001730-A1.
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17-JUL-1998;
29-DEC-1998;
                                                                                                                                                 Homo sapiens.
Synthetic,
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                                                           25-APR-2000
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                                       AAY78096;
RESULT 1
        AAY78096
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Dolphin GT;

Baltzer L,

Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

06:52:00 2003

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AAY78080 standard; Peptide; 12 AA.
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Matches
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or prevention of infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. Fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-inflectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food Claim 22; Page 38; 102pp; English.

Local Similarity 91.7

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Gaps . 0

93.8%; Score 60; DB 21; Length 12; 91.7%; Pred. No. 0.00059; ive 1; Mismatches 0; Indels

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:80.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

98SE-0002441. 98SE-0002562. 98SE-0004614,

Dolphin Baltzer L, Mattsby-Baltzer I,

New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food

Claim 22; Page 36; 102pp; English.

AAY78001 to AAY78100 represent peptides having sequences based on human

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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-linflammatory anti-linfectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 0.0066;
Mismatches 0; Indels
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ilarity 75.0%;
Conservative
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98SE-0002562.
98SE-0004614.
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29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericial and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-inflammatory bused clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin walld enable them to be used for the same purposes as lactoferrin at lower
fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumourinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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Pred. No. 0.015;
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                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; Page 38; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY78092 standard; Peptide; 12 AA
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98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                             81.2%;
75.0%;
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                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                              Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                             CFQLKKNMKKVR
                                                                                                                                                                                                                       12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-1998;
29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
AAY78092
ID AAY7
  88888888888
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment or house tract infections. Among the peptide or fragment or no be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also fungloidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
Query Match 81.2%; Score 52; DB 21; Length 12; Best Local Similarity 75.0%; Pred. No. 0.015; Matches 9; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dolphin GT
                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baltzer L,
                                                                                                                                                                                                AAY78081 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Page 36; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                        1 CFQLKKNWKKVR 12
                                                                                         1 CFQWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1998;
29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                  AAY78081;
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ID AAY7
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Gaps

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79.7%; Score 51; DB 21; Length 12; larity 75.0%; Pred. No. 0.022; Conservative 2; Mismatches 1; Indels

2;

Best Local Similarity Matches 9; Conserv

Sequence Query Match Human lactoferrin derived peptide SEQ ID NO:97.

(first entry)

25-APR-2000

AAY78097;

AAY78097 standard; Peptide; 12 AA.

1 CFQLKKNMKKVR

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and candida infection on a mucosal curinary tract infections and/or tumours. The peptides can also be used as preservatives.

C uniquidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                        modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 0.022;
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                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:83.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 36; 102pp; English.
                                                                                            AAY78083 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.7%;
75.0%;
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98SE-0002562.
98SE-0004614.
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                                                                                                                                                          (first entry)
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1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                            Human, lactoferrin;
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                                                                                                                                                                                                                                                                                                                           Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through hading to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used as the food and though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoursal properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would canble them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                             Human, lactoferrin, modification, infection, inflammation, tumou food, infant formula, anti-inflammatory, anti-microbial, anti-tum urinary tract infection; colitis; Candida infection, fungicidal, bactericidal, preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; Page 94; 102pp; English.
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98SE-0002562.
98SE-0004614.
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les 10; Conservative
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17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                               Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78071;
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Matches
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Gaps

1; Indels

2; Mismatches

9; Conservative

Matches

Query Match Best Local Similarity

1 CFQLKKNMKKVR 12

1 CFQWQRNMKKVR

RESULT 7 AAY78097

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Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                  98SE-0002441.
98SE-0002562.
98SE-0004614.
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29-DEC-1998;
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                                                                                                                                         Synthetic
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Dolphin GT;

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower 0; Gaps Score 49; DB 21; Length 12; Pred. No. 0.049; 3; Mismatches 1; Indels 76.68; Query Match

. . 8; Conservative 1 CFQLKKNWKKVR 12 Best Local Similarity Matches 8; Conserv

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||| ::||:|| CFQAQRNMRKVR 12 RESULT 9 ద

AAY78038 standard; Peptide; 12 AA.

Human lactoferrin derived peptide SEQ ID NO:38. (first entry) 25-APR-2000

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; uninary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative

Homo sapiens

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired the control of the peptides. anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower Gaps .; 0 Score 48; DB 21; Length 12; Pred. No. 0.073; 3; Mismatches 1; Indels Claim 12; Page 70; 102pp; English. 75.0%; 66.7%; 8; Conservative Query Match Best Local Similarity 12 AA; Sequence Matches

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB.

98SE-0002562. 98SE-0004614.

29-DEC-1998;

17-JUL-1998;

99WO-SE01230.

06-JUL-1999;

13-JAN-2000

WO200001730-A1

Synthetic.

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1 CFQLKKNMKKVR 12 1 CFQWQRNMRKVR 12 ઠ 셤

RESULT 10

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25-APR-2000 (first entry) AAY78046; 

AAY78046 standard; Peptide; 12 AA.

Human lactoferrin derived peptide SEQ ID NO:46.

Human, lactoferrin, modification, infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative

Homo sapiens. Synthetic.

WO200001730-A1

13-JAN-2000

06-JUL-1999;

Dolphin GT;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, collitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used to suffice and bactericidal and many also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; uxinary tract infection; colitis; Candida infection; fungicidal;
                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 21; Length 12;
Pred. No. 0.073;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:84.
Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltzer L,
                                                                                                                                          Claim 18; Page 73; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78084 standard; Peptide; 12 AA.
Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.0%;
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98SE-0004614.
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Matches 8; Conservative
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                                       WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
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29-DEC-1998;
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Hanson LA,
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                                                                                                                                        Dolphin GT;
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             98SE-0002441.
98SE-0002562.
98SE-0004614.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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Claim 22; Page 36; 102pp; English
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98SE-0004614.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as

Claim 12; Page 70; 102pp; English.

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          membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desirved anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also infood suffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

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Best Local Similarity 66.7
Matches 8; Conservative
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
usinary tract infection; colitis; Candida infection; fungicidal;
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TOPOLOGY: linear
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US-08-204-487-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-161A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-755-161A-3
US-07-755-161A-3
US-08-256-771-24
US-08-256-771-25
US-08-319-984-25
US-08-319-984-25
US-09-508-734-4
US-09-508-734-6
US-07-755-161A-10
US-07-755-161A-10
US-07-755-161A-10
US-07-755-161A-10
US-08-204-487-7
                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*
                                                                                                                                                        US-09-743-107B-96
64
                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                        1 CFQLKKNMKKVR 12
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01 W 44 r0 r0
                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                   Searched:
                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
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Appli	Appli	Appli	Appli	Appli	Appl:	Appl;	Appli											
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Sequence	Sequence	Sequence	Sequence	Segmence	Sequence	Sequence	Sequence	Segmence	Sections	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Sequence	
US-08-464-182A-2	US-08-406-271-2	US-08-724-586-2	US-09-421-632-2	US-09-932-190-2	US-08-655-640-2	US-08-655-640-4	US-08-154-019-4	US-08-461-333-4	US-08-464-167-4	US-09-158-313-4	US-08-476-798-4	US-08-145-681-2	US-08-250-308-2	US-08-453-703-2	US-08-456-106-2	US-08-456-108-2	US-09-265-577-2	
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54	54	694	694	694	705	708	711	711	711	711	711	711	711	711	711	711	711	
75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	70.3	70.3	70.3	70.3	.70.3	70.3	
4, 60	48	48	48	48	48	48	48	48	48	48	48	45	45	45	45	45	45	
28	53	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45	
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## ALIGNMENTS

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Sequence 3, Application US/08204487
Patent No. 5565425
Patent No. 5565425
Patent No. 5565425
Patent No. 5565425
Patent No. 566425
Patent No. 566425
Patent No. 566425

APPLICANT: TAMAKA, SHIGERAI
APPLICANT: TAMAKA, SHIGERAI
APPLICANT: TAMAKA, SHIGERAI
APPLICANT: TAMAKA, SHUNICHI
APPLICANT: THEBAULI
STREET: 33 STATE STREET
STREET: 33 STATE STREET
STREET: 33 STATE STREET
STREET: 33 STATE STREET
STREET: SA STATE STREET
COUNTRY: USA
COUNTRY: BADDRESSE:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURMITZ &
ADDRESSEE: PATENT ADMINISTRATOR, Version #1.25
COUNTRY: USA
COUNTRY: USA
COUNTRY: CO-DOS/MS-DOS
COUNTRY: DOS-TOWN STREET OF THE STRE
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COUNTRY: U
ZIP: 07601
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US-08-475-055-8
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: GERVIE FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
TITLE OF INVENTION: BUDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                               Score 48; DB 1; Length 18; Pred. No. 0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.0%; Score 48; 1
66.7%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
TLING DATE: APRL 7, 1995
CLASSIFICATION: WORBER: 08/418,642
FILING DATE: APRL 7, 1995
CLASSIFICATION: 436
ATTORNEY/ACENT INFORMATION:
NAME: JACKSON BEG., 26,742
REGREGRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                   UG-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: 201 5.2
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                   Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFOWORNMRKVR 12
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Best Local Similarity
                                                                                                                                              1 CFOLKKNIMKKVR 12
                                                                                                                                                                      1 CFQWQRNMRKVR 12
                                                                    Query Match
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Sequence A spalication US/0822380

Sequence A spalication US/0822380

Regent No. 5591240:

Refert No. 55912410:

REFERRATION TO THE WENDIATION OF ANTIBACTERIAL PROTEINS

NUMBER OF SEQUENCES: 9

RORRESPONDERS LADRESS 4

ADDRESSEE: Malber & Jackson Antibacterial Recent Recent
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" AUTHORS AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
NAME/KEY:
NAME/KEY:
LOCATION: 2
LOCATION: 2
LOCATION: 2
LOCATION: 0
CHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 19
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                            SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
                                                                                                 FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
TELEFAX: 202-371-8850
          OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
ORANGILE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCENTATION:
APPLICANT: Mamoru TOMITA et al.
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADERESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
STATE: D.C.
COUMTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FLING DATE:
CLASSITCATION:
PRIOR APPLICATION NUMBER: 08/485,948
PLING DATE:
APPLICATION NUMBER: 08/486,217
PILING DATE:
APPLICATION NUMBER: 08/486,217
FILING DATE: APRIL 7, 1995
CLASSIFICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
NAME: Jackson Esq., David A.
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELEPHONE: 201 343-1684
TELEPHONE: 201 343-1684
TELEFRAX: 201 343-1684
TELEFRAX: 201 343-1684
TELEROWHING CHARACTERISTICS:
LENGTH: 18 amino acids
TVPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.0%; Score 48; Best Local Similarity 66.7%; Pred. No. (Matches 8; Conservative 3; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-07-755-161A-3
; Sequence 3, Application US/07755161A
; Patent No. 5304633
                                            STREET: 411 Hackeneack Avenue
CITY: Hackeneack Avenue
CITY: Hackeneack
STATE: New Jersey
COUNTRY: USE
CONFORTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPANIEM: IBM PC COMPANIEM: PC-DOS/MS-DC
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stranger: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FRAGMENT TYPE: internal US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFOLKKNWKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQRNWRKVR 12
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"

PEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASIIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHICERALI
APPLICANT: TANAKA, SHICERALI
APPLICANT: KAWASAKI, YOSHINRO
APPLICANT: KAWASAKI, YOSHINRO
APPLICANT: VAWASAKI, YOSHINRO
APPLICANT: VIRIDA, TOSHINKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 48; DB 1; Length 20; 66.7%; Pred. No. 0.062; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTR:

COUNTR:

COUNTRE READABLE FORM:

MEDIUM TYPE: Floopy disk

COMPUTER: IBM FC Compatible

COMFUTER: IBM FC Compatible

COMFUTER: IBM FC Compatible

COMFUTER: IBM FC COMPACE

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 02-MAR-1994

CLASSIFICATION: 514

ATTORNEY AGENT INFORMATION:

NAME: CAMPBELL, PAULA A.

REGISTRATION NUMBER: 32,503

REGISTRATION NUMBER: 32,503

TELECOMMINICATION INPORMATION:

TELECOMMINICATION INPORMATION:

TELECOMMINICATION INPORMATION:

TELECOMMINICATION INPORMATION:

TELECOMMINICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATENT ADMINISTRATOR, TESTA, HURWITZ
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-204-487-1; Sequence 1, Application US/08204487; Setent No. 5565425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EANTENT ADMINI
STREET: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                            IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQLKKNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: M2
COUNTRY:
                                                                                                                                                                                                                                                                                            TITLE:
JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
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G
                            Gaps
                            ·
0
                            1; Indels
                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

ZIATE: D.C.

CONDUTRY: U.S.A.

ZIP: 20005

COMPUTER: DisKette, 5.25 inch, 500Kb

COMPUTER: DisKette, 5.25 inch, 500Kb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS.DOS

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US,07/891,174

FILING DATE: 29-MAY-1992

CLASSIFICATION: 530

PRIOR APPLICATION: 530

RIUNG DATE: US,525,161

ATTORNEY/AGENT INFORMATION:

NAME: WALTEN M. CHECK JY.

REFERENCE/DOCKET NUMBER:

TELESPHONE: 202-371-8850

TELESPAK: 202-371-8856
                          3; Mismatches
                                                                                                                                                                                    5-07-891-174-3
Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: modified site
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POSITION IN GENOME:
CHROMOSOME/SEGMENT
MAP POSITION:
                                                                 1 CFQLKKNWKKVR 12
                                                                                      | | | ::||:||
2 CFQWQRNMRKVR 13
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
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Gaps
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Patent No. 565691

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION:
ANIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
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IDENTIFICATION METHOD:

// OTHER INFORMATION: /note= "Cys residues are protected' to

OTHER INFORMATION: prevent disulfide bond"

US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 1; Length 20;
Pred. No. 0.062;
3; Mismatches 1; Indels
                                          Length 20;
                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: Ms. DOS SOFTWARE: Wordperfect 5.1 CURENT APPLICATION NUMBER: U$/08/256,771 FILING DATE: July 22, 1994 CLASSIFICATION: 514 PRIOR APPLICATION NUMBER: STILING DATE: APPLICATION NUMBER: STILING DATE: ATTORNEY/AGENT INFORMATION: NAME: WATTEN M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERRENCE/DOCKET NUMBER: 33,367 REFERRENCE/DOCKET NUMBER:
                                        Score 48; DB 1;
Pred. No. 0.062;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 STATE: 0.C. COUNTRY: U.S.A. COUNTRY: U.S.A. COUNTRY: U.S.A. COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
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Best Local Similarity 66.7%;
Matches 8; Conservative
                                          Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth
                                                                                                                             1 CFQLKKNMKKVR 12
                                                                                                                                                  2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQLKKNMKKVR 12
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US-08-381-984-24
  US-08-256-771-24
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Fatent No. 5656591
GENERAL INFORMATION:
FAPLICANT: MAMOOT TOWITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wanderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Mashington
STATE: D.C.
COMPTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: Mordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                        NAME/KEY: Peptide
LOCATION: 1..20
OTHER INPORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                   Score 48; DB 1;
Pred. No. 0.062;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT ADLUCTUC 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/25
FILING DATE: JULY 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J.
REGISTRATION NUMBER: 33,
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER
                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                             MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQLKKNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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Patent No. 6423509
| Sequence 4, Application US/09508734
| Sequence 4, Application US/09508734
| Patent No. 6423509
| GENERAL INPORMATION:
| APPLICANT: Samyang Genex Corporation
| TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
| TITLE OF INVENTION: useful microorganism thereof
| TITLE OF INVENTION: useful microorganism thereof
| TITLE OF INVENTION: useful microorganism thereof
| FILE REFERENCE: PA/SYG/00139
| CURRENT APPLICATION NUMBER: US/09/508,734
| PRIOR APPLICATION NUMBER: EVT/KR99/00373
| PRIOR APPLICATION NUMBER: KR1998-29351
| PRIOR PRIING DATE: 1999-07-14
| PRIOR FILING DATE: 1999-07-13
| NUMBER OF SEQ ID NOS: 12
| SOFTWARE: KopatentIn 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment there
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMBUTER: Diskette, 3.5 inch, 1.44 mb
COMBUTER: Diskette, 3.5 inch, 1.44 mb
COMBUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION NUMBER: 1995
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: WALFEN M. Cheek, Jr.
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELESHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 1;
Pred. No. 0.062;
3; Mismatches
: 805 Fifteenth Street, N.W., #700 Washington
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CFOWORNMRKVR 13
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                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino a
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                      COUNTRY:
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LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 48; DB 1; Length 20; 66.7%; Pred. No. 0.062; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible OPERATUS SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
TALORNEY/AGENT INFORMATION:
NAME: WATER MY Check, UT.
REGISTRATION NUMBER: 33.367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAX:
TELE
Sequence 24, Application US/08381984
Patent No. 580455
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
STATE: 20055
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Sequence 25, Application US/08381984;
Patent No. 580455;
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQLKKNMKKVR 12
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Matches 8, Conserv
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NAME/KEY:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "thiol group of Cys residue at location 4 connected by disulfide bond with thiol group of Cys residue at location 21"
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PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                   NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAK: 202-371-8856
                                                                                                                                                                          10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION:
LOCATION:
                                                                                                                                         INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 25 anino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REATURE:
NAME/KEY: modified site
LOCATION: 21
FILING DATE:
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
HYPOTHETICAL:
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
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                                                                                                                                                                                                                                                                   ESULT 13
IS-09-508-734-6
IS-09-508-734-6
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENITON: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENITON: useful microorganism thereof
FILE REPRENEUE: PASYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
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                                                                                            Query Match 75.0%; Score 48; DB 4; Length 22; Best Local Similarity 26.7%; Pred. No. 0.068; Matches 8; Conservative 3; Mismatches 1; Indels
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JS-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Agent
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendercth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STANDER: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
ZIF: 20005
COMPUTER READABLE FORM:
REDIUM TYPE: DISKELEE, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SSCTWARE: KOPAtentin 1.71
LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: DisplayWrite CURRENT APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
IS-09-508-734-6
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
IS-09-508-734-4
                                                                                                                                                                          1 CPOLKKNIMKKVR 12
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Gaps

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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Oys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB 1; Length 25;
Pred. No. 0.077;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                 DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative 3
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ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL TYPE:
CELL TYPE:
CELL TYPE:
CERL TYPE:
CRANDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHANDIANE:
CHANDIANE:
NAME/KEY: modified site
LOCATION:
WARP/KEY: modified site
LOCATION:
CATHER INFORMATION: //note= "thiol group of OTHER INFORMATION: thiol group of Cys residue at location 2"
DOTHER INFORMATION: thiol group of Cys residue at location 2"
             NESCULT 15

19.5-07-101-174-10

19.5-07-191-174-10

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Sequence 202, App
Sequence 244, App
Sequence 4127, A
Sequence 2488, App
Sequence 21, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 1248, Ap
Sequence 1248, Ap
Sequence 1248, Ap
Sequence 1248, Ap
Sequence 1248, Appl
Sequence 11530, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 37, Appl
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0 US-09-071-838-202

0 US-09-764-86-244

0 US-09-764-853-738

0 US-09-764-853-738-11

0 US-09-766-692-2458

0 US-09-927-107-33

0 US-09-987-107-33

0 US-09-987-107-34

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0 US-09-981-875-12

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US-09-866-562-37
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US-10-155-789-4
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Publication No. US20030022821A1

GENERAL INFORMATION:

APPLICANT: GVSTEIN REKDAL

APPLICANT: (VSTEIN REKDAL

APPLICANT: (VSTEIN REKDAL

APPLICANT: LARS VORLAND

APPLICANT: LARS VORLAND

TILLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: CB9818938.4

PRIOR PILING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SEQ ID NOS: SEQ ID NOS: 30

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
      8; Conservative
                                                                                                                                                  429
470
1499
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CORGANISM: HOMO SAPIENS
US-09-798-869-2
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Matches 8; Conserv
    US-09-798-869-20
    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Appli
Sequence 20, Appl
Sequence 5, Appli
Sequence 6, Appli
Sequence 16, Appli
Sequence 37163, A
                                                                                                  February 21, 2003, 08:08:15; search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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(ggm2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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(ggm2_6/ptodata/2/pubpaa/USO6_PUBGOMB.pep:*

(ggm2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

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(ggm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

(ggm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:* / /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*
               5.1.3
Compugen Ltd.
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US-10-09-798-869-2
US-10-02-09-869-6
US-09-798-869-6
US-09-98-85-655B-16
US-09-98-96-981-5
US-09-96-981-5
US-09-96-981-5
US-09-96-981-5
US-09-81-132-599
US-09-81-132-599
US-09-864-761-43420
US-09-81-588-4
US-09-81-588-4
US-09-81-588-4
US-09-81-588-4
US-09-81-588-4
US-09-81-588-4
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US-09-81-588-4
US-10-046-933-2235
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US-09-764-877-1902
US-09-864-761-40172
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                   156504 segs, 31069816 residues
                 GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                         US-09-743-107B-96
                                                                                                                                                                                                                                                                                                                          Winimum DB seq length: 0 Waximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                               Jatabase
                                                                                                     Run on:
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No.
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Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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                                                                                                     22 CFOWQRNMRKVR 33
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US-09-853-625B-16
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Patent No. US20020160941A1

GENERAL INFORMATION:

APPLICANT: Kruzel, Marian L.

APPLICANT: GLINICK, Paul D.

APPLICANT: GLINICK, Paul D.

APPLICANT: COUNTION: Lactoferrin

ITLE OF INVENTION: Lactoferrin

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPER: 400 Seventh St. N.W.

CITY: Washington D.C.

COUNTY: U.S.A.

ZIP: 2004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PRECENTION RELEASE #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/023,096
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                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                       TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-28
                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 30
SOFTWARE FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Player, William E. REGISTRATION NUMBER: 31,409 REPERENCE/DOCKET NUMBER: 10: TELECOMMUNICATION: 1838-6666
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7%;
Matches B; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 694 amino acids
amino acid
          LARS VORLAND
                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
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US-10-023-096-2
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Quest March

Desire Local Signalization 75.14, Score 48, pp 9; Length 694;

Matchee B; Connervative 3; Mismatches 1; Indels 0; Gaps 0;

1 CPOLECOMMENT 12

Desire Connervative 3; Mismatches 1; Indels 0; Gaps 0;

2 CPORGENMENT 33

RESULT 4

RESULT 4

RESULT 4

RESULT 4

RESULT 1.188 OF INVENTIVE SPETIDES

FILE RESERVED IN STRIND INSTRUMENT SPETIDES

FILE RESULT SPETI
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CTHER INFORMATION: EXPRESSED IN BALIN, SIGNAL = 9.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN BAT44, SIGNAL = 7.5

OTHER INFORMATION: EXPRESSED IN BAT44, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BOTE LIVER, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BOTE ANAROW, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.7

OTHER INFORMATION: STATEMENT HUMAN HIT: O07920, EVALUE 1.00e-26

US-09-864-761-37163
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                                PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION UNDABER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEG TWARRS: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 37163
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 345, Application US/09574879
Sequence 345, Application US/09574879
Publication No. US20030028003A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REPERENCE: PZ020P2
CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR PILLING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR FILING DATE: 2000-10-13
PRIOR PELICATION NUMBER: US 09/305,736
PRIOR PELICATION NUMBER: US 09/305,736
PRIOR FILING DATE: 1999-05-05
PRIOR FILING DATE: 1999-11-04
PRIOR FILING DATE: 1997-11-07
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APPLICATION NUMBER: US 60/064,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/064,988
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PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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OTHER INFORMATION:
OTHER INFORMATION:
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Patent No. US20200487631

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPERENCE: Acomica. X.1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-02-04
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Pred. No. 7.7;
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                                                                                                              REFERENCE/DOCKET NUMBER: 325800-442
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN SEQ ID NO: 16: S-09-853-6258-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-01-30
RRICR APPLICATION NUMBER: PCT/USC1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USC1/00662
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00669
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PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LICATION NUMBER: US 60/236,359
                             ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                    LENGTH: 351 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
     FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.6%;
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Best Local Similarity 66.7
Matches 8; Conservative
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IS-09-864-761-37163
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Gaps

us-09-743-107b-96.rapb

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Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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US-10-007-693-107
        US-09-841-132-599
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PRETENT NO. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Brakiky, Yasir A.W.
APPLICANT: Schiky, Yasir A.W.
APPLICANT: Schiky, Manay
APPLICANT: OMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210.12.465C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FREESE FREESE FOR Windows Version 3.0/4.0
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Pred. No. 1.1e+02;
1; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: US 60/066,100
PRIOR FILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-17
PRIOR PELLING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-17
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 611
SSOFTWARE: PatentIn Ver. 2.0
SSOTTMARE: 28
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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CRGANISM: Homo sapiens
US-09-905-983-52
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LENGTH: 358
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Sequence 43420, Application US/09864761

Patent No. US200200487631

GENERAL INFORMATION:

APPLICAMT: Penn, Sharron G.

APPLICAMT: Hanzel, David R.

APPLICAMT: Hanzel, David K.

APPLICAMT: APPLICAMT: Hanzel, David K.

APPLICAMT: Chen, Wensheng

TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR PRINCE DATE: 2001-02-04
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                                                                                                                                                                                                                                                                                                                    ; Sequence 107, Application US/10007693
; Patent No. US20020146776A1
; GENERAL INFORMATION:
   APPLICANT: Bhatia, Ajay
   APPLICANT: Probert, Peter
   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT:
   TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
   FILE REFERENCE: 210121.515C2
; CURRENT APPLICATION NUMBER: US/10/007,693
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.2%; Score 36; DB 12; Length 358; 60.0%; Pred. No. 75; ive 2; Mismatches 2; Indels
56.2%; Score 36; DB 10; Length 358; 60.0%; Pred. No. 75;
                                                           2; Mismatches
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-07
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ; ORGANISM: Chlamydia trachomatis serovar D US-10-007-693-107
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Secrist, John A.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.5270;
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2235
LENGTH: 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 10; Length 347; Pred. No. 1.5e+02; 1; Indels 3; Mismatches 1; Indels
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                                                                                                                        Sequence 4, Application US/09851588

Patent No. US20020042067A1

GENERAL INFORMATION:

APPLICANT: Mack, David

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COL

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CA

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CA

FILE REFERENCE: A-68829-1/DuB/JUD/AMS

CURRENT APPLICATION NUMBER: US/09/851,588

CURRENT FILING DATE: 2001-09-24

PRIOR PILING DATE: 2000-08-17

PRIOR PILING DATE: 2000-08-17

PRIOR PILING DATE: 2000-09-17

PRIOR FILING DATE: 2000-09-17

PRIOR PILING DATE: 2000-09-17

PRIOR PILING DATE: 2000-09-17

PRIOR PLING DATE: PARMING NUMBER: US 09/656,002

PRIOR PRIOR PRIOR PRIOR NUMBER: US 09/656,002

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PRIOR PRIOR PRIOR NUMBER: US 09/656,002
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60.0%; Pred. No. 1.6e+02;
tive 3; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2235, Application US/10046935
Patent No. US20020156011A1
GENERAL INFORMATION:
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Best Local Similarity 60.0°
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ORGANISM: Homo sapiens
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Best Local Similarity
'''n 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-046-935-2235
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Patent No. US20020042385Al

GENERAL INPORMATION:
APPLICANT: Bergsman Derk S.
APPLICANT: Elshourbagy, Nabil
FILLS OF INVERTION CLONING OF A NOVEL 7TM RECEPTOR AXOR-2
FILLS OF INVERTION OF SEQ. 105,336
PRIOR APPLICATION NUMBER: US 09/277,398
PRIOR PLING DATE: 1999-03-26
PRIOR PLING DATE: 1999-03-26
SEQ ID NO 2
LENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 10; Length 373;
Pred. No. 1.1e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BOLLT LIVER, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: POS458, EVALUE 4.80e+00
3-09-864-761-43420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.7%; Score 35; DB 10; Length 46; 63.6%; Pred. No. 16; 1.1ve 1; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43420
LENGTH: 46
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 63.6
Matches 7; Conservative
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ORGANISM: HOMO SAPIENS
:-09-760-354A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: M
OTHER INFORMATION: E
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OTHER INFORMATION: E
OTHER INFORMATION: E
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RESULT 15

340 CFLLNKDLKK 349

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US-09-878-178-235

Sequence 2225, Application US/09878178

Sequence 2225, Application US/09878178

Sequence 2225, Application US/09878178

Sequence 2225, Application US/09878178

APPLICANT: Jang, Yuqiu

APPLICANT: Secriet, Heather

APPLICANT: Secriet, Heather

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

ITILE OF INVENTION: COMPOSITIONS OF COLON CANCER

FILE REFERENCE: 21012.1.52

CURRENT APPLICATION NUMBER: US/09/878,178

CURRENT PALLIG DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 2237

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 371

TYPE: PRT

ORGANISM: Home sapiens

FEATURE:

NAME/KEY: variant

LOCATION: (1) ... (371)

CUTHER INFORMATION: Xaa = Any amino acid

US-09-878-178-2235

OUBEY MATCh

SS 3.1%; Score 34; DB 9; Length 371;

Best Local Similarity 60.0%; Pred. No. 1.6e+02;

MATCHES 6; Conservative 3; Mismatches 1; Indels 0; Gaps
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Search completed: February 21, 2003, 08:11:58 Job time : 6.88372 secs

12 RVKKNLKKFR 21

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O H O M	4.10.0	or & & & &	⊃ H (1) (M °	4 ብ 4 ቢ		E E	TEHUL lactotransfer	C;Species: Hc C;Date: 31-Ma C;Accession:	R;Cho, Y. submitted to A;Reference r A;Accession: A;Catus: pre A;Molecule ty	A; Residues: 1 A; Cross-refer R; Rey, M.W.; Nucleic Acide	A;Title: Comp A;Reference I A;Accession:	A; Molecule ty A; Residues: 1	R;Teng, C.T.;	A; Title: Diff	A; Accession:	A; Molecule Ly A; Residues: 1	A, Cross-refer A, Experimenta	A; Note: seque	Nucleic Acids	A;Reference r	A, Molecule ty	A; Cross-refer	R;Stowell, K. Biochem. J. 2	A,Title: Expr	A; Accession:	A;Status: nuc A;Molecule ty	A;Residues: 2 A;Accession:	A;Molecule ty A;Residues: 2
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version 5.1.3 - 2003 Compugen Ltd.	1e]	:01 ; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec			residues	1rameters: 283224				<pre>predicted by chance to have a e score of the result being printed, total score distribution.</pre>	SUMMARIES	Description	transfe	procein . Othetical passing	hypothetical prote	rna binding protei	N	secY protein - red hypothetical prote	hypothetical prote	hypothetical prote similar to ch-TOG	secretory protein	hypothetical prote	hypothetical prote conserved hypothet	conserved hypothet	cadherin 5 precurs	hypothetical prote hypothetical prote	hypothetical prote cell filamentation	hypothetical prote hypothetical prote
GenCore veri Copyright (c) 1993 - 20	in - protein search, using sw model	February 21, 2003, 07:48	US-09-743-107B-96 score: 64 :: 1 CFQLKKNNKKVR 12	table: BLOSUM62 Gapop 10:0 , Gapext 0.5	: 283224 seqs, 96134422	number of hits satisfying chosen parameters	DB seq length: 0 DB seq length: 200000000	ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	: PIR 73:* 1: Dirl:* 2: pir2:* 3: pir3:* 4: pir4:*	Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the t		Query Score Match Length DB ID	75.0 711 1	42 65.6 795 2 T34468 40 60.6 703 2 T34468	62.5 238 2	60.9	9 60.9 339 2	9 60.9 409 2 9 60.9 1162 2	9 60.9 1553 2 8 59.4 1166 2	59.4 2014 2 59.4 2021 2	7 57.8 22 2	7 57.8 267 2	7 57.8 335 2 7 57.8 510 2	7 57.8 546 2	7 57.8 784 1	6 56.2 81 2 6 56.2 81 2	6 56.2 104 2 6 56.2 191 2	6 56.2 227 2 6 56.2 258 2
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hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	B. subtilis DeoR t	probable p-loop AT	hypothetical prote	arginine-tRNA liga	hypothetical profe	hypothetical prote	hypothetical prote	Ca2+-transporting	hypothetical profe	hypothetical prote	hypothetical prote	hypothetical prote
T00446	S50454	S49781	D86255	AD1143	D71533	T22121	F64329	T15710	A96516	A99334	T18294	F90520	T22965	G90017	C90107
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30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45
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hypothetical prote B. subtilis Deox t probable p-loop AT hypothetical prote arginine-tRNA liga hypothetical prote hypothetical prote hypothetical prote Ca2+-transporting hypothetical prote	ALIGNMENTS	- human 21-Nov-1997 #text change 08-Dec-2000 0324; S15853; S20841; S07160; A61169; A31000; S741	r, March 1994 from GB/EMBL/DDBJ	A;Residues: 1-711 <cho>A;Residues: 1-711 <cho>A;Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237 R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. Nucleic Acids Res. 18, 5288, 1990</cho></cho>	human mammary giand iactoferrin. ; PMID:2402455 «RRY»	; PIDN:CAA37914.1; PID:g34416 ; Panella, T.	of the estrogen action that regulates lactofer: ; PMID:1480183	A;Residues: 1-15 <ten> A;Cross-references: GB:852659; NID:g263311; PIDN:AAB24877.1; PID:g263312 A;Experimental source: Dlacenta</ten>	oone (NCBIP:122202)	coferrin cDNA. ; PMID:2374734	11; PIDN:CAA37116.1; PID:934412	ochem. J. 276, 349-355, 1991 Title: Expression of cloned human lactoferrin in baby-hamster kidney cells. Reference number: S15853, MUID:91264786; PMID:2049066	; not compared with conceptual translation	Carte Cond
D86255 AD1143 AD1143 T122121 T122121 T15710 T15710 T15710 T15710 T15294 T122965 C90107	ALIGN	[validated] - hum rin n) ce_revision 21-No ; A45401; S10324;	7, March   from GB,	NID:g467 er, H.A.	Alfille: Complete nucleotide sequence of R Alfeference number: S11228; WUID:90384839; Alfocession: S11228 Alfocession: S11228 Alfeseidines: 1-148, TV:150-422, CV:424-711	NID:9344 Walmer,	A,Title: Differential molecular mechanism of A,Reference number: A45401; MUID:93125571; A,Accession: A45401 A,Molecule type: DNA	D:926331	ICBI back	uman lac 90326549	NID:9344	n lacto 91264786	on: \$19853 nucleic acid sequence not shown; not e type: mRNA e: 20-31 <\$T1> on: \$20841	,
ппинипининин		alić n rev 7454	Library, slated f	13; 1eBc 1990	다. 	11.7	μπ JID:	Ϋ́ e	E O	NE P	#1.7 Punt	T di	e e	<st2></st2>
299 3315 3315 660 1086 1109 1109		ecursor [valactoferrin lactoferrin piens (man)   #sequence     S11228   A	Data Library 1820 translated	E: U0764 8.L.; C	228; MT 50-422.	EMBL:X53961; Y.; Yang, N.; , 1969-1981, 1	olecula 401; MT	852659; placent	ited fro	uence o	II:X5294	5, 1991 cloned 853; MU	seguenc	
		n precurse: lact sapient 1992 #se	the EMBL GOOD 100 CO	11 < CHO; ses: EME loshuk, ss. 18,	e nucle er: S11 228 mRNA	u, Y.; 6, 196	ential noer: A45 8401 DNA	<pre>c TEN&gt; ses: GB: source:</pre>	extrac Ogden,	ide sec oer: S10	mRNA 1 < POW>	349-35 sion of ser: S15	1: S15853 nucleic acid type: mRNA 20-31 <st1> 1: S20841</st1>	type: protein 20-28,'X',30-31
<b>๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛</b>		RESULT 1 THUL lactotransferrin precursor [v N;Alternate names: lactoferri C;Species: Hono sapiens (man) C;Date: 31-Mar-1992 #sequence C;Accession: G01394; S11228;	submitted to the EMBL Data A;Reference number: G06820 A;Accession: G01394 A;Status: preliminary; trai A;Wolecule type: mRNA	reference. 1-71 reference. Wol Acids Re	A,Title: Complete nuc. A,Reference number: S. A,Accession: S11228 A,Molecule type: mRNA A,Residues: 1-148.'T.	referenc C.T.; Li locrinol.	A;Title: Differenti A;Reference number: A;Accession: A45401 A;Molecule type: DN	les: 1-15 referenc mental g	sequence, M.J.;	Nucleot noe numb	A; Molecule type: mRNA A; Residues: 3-711 < POW> A; Cross-references: EMBI	J. 276, Expressince numb	ion: Sis i: nuclei ile type: es: 20-3 ion: S20	le type: es: 20-2
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Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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Matches
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A)Cross-references: GDB:119368; OMIM:150210
C)Superfamily: transferrin; transferrin repeat homology
C)Superfamily: transferrin; transferrin in iron binding; milk
C)Superfamily: transferrin; dycoprotein; iron binding; milk
C)1-13/Domain: signal sequence #status predicted <81G>
F)2-11/Product: lactotransferrin #status experimental <AMT>
F)2-356/Domain: transferrin repeat homology <ARH2>
F)2-356/Domain: transferrin repeat homology <ARH2>
F)2-65,33-56,135-218,177-193,190-201,251-265,503-697,555-609/Disulfide bonds: #status F)356-808/Binding site: carbohydrate (Asn) (covalent) #status experimental
F)368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #status
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Species: Gallus gallus (chicken)

Species: Gallus gallus (chicken)

Species: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000

Joliot. V.; Martinerie, C.; Dambrine, G.; Plassiart, G.; Brisac, M.; Crochet, J.; Perb. (cl. Cell. Biol. 12, 10-21, 1992)

Fittle: Proviral rearrangements and overexpression of a new cellular gene (nov) in myelly Reference number: S20078; MUID:92107157; PMID:1309586
                                                                                                                                                                  Residues: 3-701, SWKPVN' <PAN>
Experimental source: normal breast tissue
Metz-Boutique, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Metz-Boutique, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
M.T. Biochem. 145, 659-666, 1984
Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
Reference number: A31000; MUID:85076667; PMID:6510420
Accession: A31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: protein

Residues: 20-140,142-159,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
Residues: 20-140,142-159,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
Note: this is the final paper in a series
Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Rr. J. Blochem: 241, 303-308, 1996
Tritle: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
Reference number: S74119; MUID:97054624; PMID:8898921
                                                                               Ę
,Rado, T.A.; Wei, X.; Benz Jr., E.J.
Lood 70, 989-993, 1987
.Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of ;Reference number: S07160; MUID:88001031; PMID:3477300
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Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                       Status: not compared with conceptual translation Molecule type: mRNA
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tesidues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
Experimental source: neutrophil granulocytes
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Molecule type: mRNA
Residues: 1-351 <JOL>
                                                                                                                                                                                                                                                                                                                                                                                         Accession: A61169
                                                                                                                                    Accession: S07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cession: S74119
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A,Map position: 1
A,Introns: 18/1; 84/2; 125/3; 198/3; 257/3; 337/3; 378/3; 424/3; 477/2; 510/1; 563/3; 63
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A;Molecule type: DNA
A;Molecule type: DNA
A;Status: 1-223 AMUR.
A;Status: Tagas AMUR.
A;Cross-references: EMBL:269909; PIDN:CRA93785.1; GSPDB:GN00066; SPDB:SPAC19G10.03c
A;Experimental source: strain 972h-; cosmid c19G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable peroxisomal membrane protein - fission yeast (Schizosaccharomyces pombe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: 134468
R.Maggl, L.; Gattung, S.; Bartko, L.
A.Description: The sequence of C. elegans cosmid ZK770.
A.Description: The sequence of C. elegans cosmid ZK770.
A.Accession: 134468
A.Accession: T34468
A.Accession: T3468
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C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C.Accession: T37974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                    Gaps
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A,Introns: 10/3,170/2
C,Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
C,Keywords: peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, March 1996
A.Reference number: Z21759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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Pred. No. 20;
2; Mismatches 1; Indels
Length 351,
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                                                                                                    3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Caenorhabditis elegans
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7
     Score 42; DB 2
Pred. No. 9.5;
1; Mismatches
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Pred. No. 14;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y match
Local Similarity 70.0%;
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pothetical protein ZK770.1
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Gaps

m

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uncharacterized conserved protein CAC2549 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 #Sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 #Second 397214

R;Nolling, J.; Breton, G.; Cmelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.

J; Bacteriol. 183, 4823-4834, 2001

A;Hitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359125; PMID:21359125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA_
A,Residues: 1-282 <KUR>
A,Cross-references: GB:AE001417; PIDN:AAK80500.1; PID:g15025572; GSPDB:GN00168
A,Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CAC2549
C;Superfamily: Deinococcus radiodurans hypothetical protein DRB0099
                                                                                                                                                                                                                                  Query Match 60.9%; Score 39; DB 2; Length 222; Best Local Similarity 100.0%; Pred. No. 21; Matches 8; Conservative 0; Mismatches 0; Indels
                A;Cross-references: EMBL:AL162875
A;Experimental source: cultivar Columbia; BAC clone T32M21
C;Genetics:
                                                                                                       A,Map position: 5
A;Introns: 38/3; 78/1; 96/3; 112/3; 145/2; 168/3; 205/3
A;Note: T32M21.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 2;
Pred. No. 26;
3; Mismatches
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Best Local Similarity 58.3
Matches 7; Conservative
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A, Genome: nucleomorph
C, Keywords: nucleomorph
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                 4 LKKNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                     9 LKKNMKKV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Genetics:
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Alternate names: protein T32M21.200
Alternate names: protein T32M21.200
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
Accession: T48456
Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De ies, H.W.; Rudk, S.; De clerck, R.; Mayer, K.F.X.
Deniced to the Protein Sequence Database, March 2000
Reference number: 22448?
                                                                                                                                                                                                                                                                                                               Residues: 1-218 <WOO>
Cross-references: EMBL:AL096788; PIDN:CAB46672.1; GSPDB:GN00067; SPDB:SPBC582.09
Experimental source: strain 972h-; cosmid c582
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Experimental source: strain Bristol N2; clone F48D6
oothetical protein SPBC582.09 - fission yeast (Schizosaccharomyces pombe)
Species: Schizosaccharomyces pombe
Nate: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
Accession: T29242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         introns: 15/3; 25/3; 185/2
Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
                                                                                         Accession: T40568
NACCESSION: T40568
NA.; Barrell, B.G.; Davis, P.; Churcher, C.M.
Dibnitted to the EMBL Data Library, July 1999
Accession: T40568
Scatus: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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62.5%; Score 40; DB 2; Length 238;
Best Local Similarity 41.7%; Pred. No. 15;
Matches 5; Conservative 6; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Map position: X
Introns: 46/3; 95/3; 121/3; 173/3; 212/3; 266/2; 302/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geisel, C.; Bradshaw, H.
bmitted to the EMBL Data Library, May 1996
Description: The sequence of C. elegans cosmid F48D6.
Reference number: 220593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pothetical protein F48D6.2 - Caenorhabditis elegans
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Status: preliminary; translated from GB/EMBL/DDBJ
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155 CYELQQNSKKIK 166
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198 CFLIRKNWKRVK 209
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Molecule type: DNA
Residues: 1-222 <BEV>
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Gene: CESP: F48D6.2
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Gaps

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2; Indels

Length 282;

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hypothetical protein orf339 [imported] - Guillardia theta nucleomorph G.Species: nucleomorph Guillardia theta
G.Species: nucleomorph Guillardia theta
G.Species: nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
G.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C.Accession: D90106
G.Accession: D90106
May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
G.Accession: D90106
A.F. Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reit
A.F. File: The highly reduced genome of an englaved algal nucleus.
A.Reference number: A99082; MUID:11323671; PMID:11323671
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A,Molecule type: DNA
A,Residues: 1-339 <DOU>
A;Residues: 1-339 <DOU>
A;Cross-references: GB:AJ010592; NID:g12580683; PIDN:CAC27001.1; GSPDB:GN00151
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.9%; Score 39;
80.0%; Pred. No.
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Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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Matches 7; Conserv
                                                                                                                                                                                                                        39 MKKNMKKVK 47
                                                                                                                                                                                      4 LKKNMKKVR 12
     A, Map position: 3
A, Note: C0755c
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A;Introns: 51/1;-78/1; 132/2; 161/1; 236/3; 276/3; 295/3; 318/3; 359/3; 397/3; 470/3; 54
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A;Molecule type: DNA
A;Molecule type: DNA
A;Across-references: GMIL: 278543; PIDN: CAB01753.1; GSPDB:GN00028; CESP:F29G6.1
A;Experimental source: clone F29G6
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;Cross-references: EMBL:Z98551; NID:e1331903; PID:e1331923; PIDN:CAB11141.1
                                                                                                                                                     secY protein - red alga (Cyanidium caldarium)
C;Species: Cyanidium caldarium
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
Accession: T21557
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
Accession: T18502
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A, Molecule type: DNA
A, Residues: 1-409 <VOG>
A, Cross-references: EMBL: 236235; NID:9529651; PIDN: CAA65270.1; PID:9529652
C, Superfamily: preprotein translocase secy
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60.9%; Score 39; DB 2; Length 409;

Best Local Similarity 60.0%; Pred. No. 36;

Matches 6; Conservative 2; Mismatches 2; Indels

    Caenorhabditis elegans

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.;Molecule type: DNA
                                                                                                                                                                                                               C;Accession: S47440
R;Vogel, H.; Valentin, K.
submitted to the EMBL Data Library, August 1994
A;Reference number: S47440
A;Accession: S47440
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submitted to the EMBL Data Library, August 1996
A.Accession: T21557
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ubmitted to the EMBL Data Library, August 1997;
Reference number: Z18935
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Best Local Similarity 50.0
Matches 6; Conservative
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179 FNLKKNKKKV 188
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 113 cHAI>
R;Music, F; Gagaswara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Natures 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsferin, G.; Krodh, S.; Kunita, K.; Lapdadus, A.; Laiu, H.; Masuda,
K; Lapdadus, A.; Lazarevic, V.; Ecvine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Schoreter, R.; Stoche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sato, Sato, T.; Sato
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NResidues: 1-1166 < KGO>
NREsidues: 1-116 < KGO
NREsidues: 
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. Bacteriol. 173, 3644-3655, 1991
.jtitle: Cloning, sequencing, and expression of Bacillus subtilis genes involved in ATP-
;Reference number: A39432; MUID:91267926; PMID:1646786
;Accession: A39432
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;Experimental source: strain 168
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.Date: 21-Feb-1992 #sequence revision 21-Feb-1992 #text_change 02-Feb-2001
.Accession: A39432; S61272; A69583
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No. 1.4e+02; Conservative 2; Mismatches 2; Indels
                 Length 1553;
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Score 39; DB
Pred. No. 1.20
2; Mismatches
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Towas Joint A. S. Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., D. Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Tre 402, 761-768, 1999

tle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. Fersance number: A84420; MUID:20083487; PMID:10617197

atus: preliminary
lecule type: DNA

lecule type: DNA
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trons: 10/2; 91/3; 136/1; 159/2; 182/3; 203/1; 225/3; 280/1; 422/3; 466/3; 559/3;
722/1; 1779/3; 1843/3; 1908/2; 1941/2; 2007/2
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lecule type: DNA
sidues: 1-2014 «MIL»
sidues: 1-2014 «MIL»
ses-references: BMBL:278543; PIDN:CAB01757.1; GSPDB:GN00028; CESP:T25C12.3
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sss-references: EMBL:293779; PIDN:CAB07849.1; GSPDB:GN00028; CESP:T25C12.3
perimental source: clone H06K08
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lecule type: DNA
sidues: 1-2014 «4013»
oss-references: EMBL:Z66566; PIDN:CAA91487.1; GSPDB:GN00028; CESP:T25C12.3
perimental source: clone T25C12
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thetical protein T25C12.3 - Caenorhabditis elegans
ecise: Caenorhabditis elegans
Le: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 18-Feb-2000
cession: T21560; T23053; T25270
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te: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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st Local Similarity 87.5%; Pred. No. 2.3e+02;
tches 7; Conservative 1; Mismatches 0;
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Lited to the EMBL Data Library, November 1995
lerence number: 220007
lerence number: 725270
lession: T25270
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Search completed: February 21, 2003, 08:02:51 Job time: 12.6047 secs escherichia

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Cho Y.Y.;
Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Contains: Lactoferroxin A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Mammary gland;
MEDLINE=90364639; PubMed=2402455;
Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Liang Q., Jimenz-Flores R., Richardson T.;
Liang Q., Jimenz-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16785; Q16786; Q16789; O00756; Q9H1Z3; Q96KZ4;
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Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region
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TISSUE-Mammary gland;
TISSUE-Mammary gland;
TISSUE-Animary gland;
"Cheng H., Chen X., Huan L.;
"CDNA cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases
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VNUC_INBAD
VNUC_INBAD
VNUC_INBSI
D170_HUMAN
HEPA_HSV7J
RPOD_CHLVU
                                          YG1B YEAST
SRB3 BRARE
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  SEQUENCE FROM N.A.
TISSUE=Mammary gland;
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                                                                                                                                                 February 21, 2003, 07:28:06; Search time 5.2093 Seconds (without alignments) 95.544 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd.
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YEA5_YEA5T
TRMU_CHLTR
VNUC_CHLTR
SYR_METJA
BGLJ_ECOLI
NUC_BORBU
NUC_BORBU
RECF_TREPA
SRB3_HUMAN
SRB3_RAT
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ADDB_BACSU
Y125_MYCCA
Y504_BORBU
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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansaria A., Mardis E., Schutz K., Chen C.N., La Bastied M., Kaplan N., Greco T., Touchman J., Mazny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Diazapan Y., Glacalone J., Pae A., Powell E., Solinsky K.A., Desilva U. Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
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MEDLINE-82046817; PubMed-6794640;
METZ-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 609-711.
MEDLINE-82262043; PubMed=7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopolesis.";
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MEDLINES B8005667; PubMed-6510420;
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Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
Eur. J. Biochem. 145:659-666(1984).
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"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "An 88 amino acid long C-terminal sequence of human
                                                  Powell M.J., Ogden J.E., "Nucleotide sequence of human lactoferrin cDNA."; Nucleic Acids Res. 18:4013-4013(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 670:243-254(1981).
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                   IISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97156796; PubMed=9003186
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EBS Lett. 142:107-110(1982).
SEQUENCE OF 3-711 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                Jolles P.;
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                                                                                                                                                                                                                                                                                                                                                           Kilitworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
A Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
B. Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
E. Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.;
Mol. Vision 4:31-32(1998).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBOWATE.
-!- FUNCTION: LACTOFERROXIN A, BAND C HAVE OPIOID ANTAGONIST
ACTIVITY: LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
                                                                                                                                                                                                                     MEDLINE-91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
'Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                         Jameson G.B., Anderson B.F., Vorris G.E., Thomas D.H., Baker E.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i-SUBCELLUTAR LOCATION: Secreted.
-i-DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i-SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
                                                                                                                                                                                                                                                                           from human lactoferrin.";
Agric. Biol. Chem. 54:1803-1810(1990).
                                              Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                        CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X53961; CAA37914.1; --
EMBL; U07643; AAB60324.1; --
EMBL; M93150; AAA36159.1; --
EMBL; M83205; AAA59511.1; --
EMBL; M83205; AAA58656.1; --
EMBL; M18642; AAA8665.1; --
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X52941; CAA37116.1; -.
U95626; AAB57795.1; -.
                                                                                                                                                                                                                                                                                                                                 VARIANTS THR-30 AND ARG-48
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1LCT; 31-OCT-93.
1LFG; 31-JUL-94.
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                                                                                                                                                                                                                                                                                                                                                    PubMed=9873069;
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PDB;
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08-MAR-96. 12-MAR-97. 21-APR-97.

X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). MEDLINE=99190892; Pubmed=10089347;

1LFI; 31-OCT-93 1LGB; 31-AUG-94

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Mol. Cell. Biol. 12:10-21(1992)
Mol. Cell. Biol. DEPRESSION OF A N-TERMINAL-TRUNCATED WITH
TUNCRIGENESIS AND EXPRESSION OF A N-TERMINAL-TRUNCATED VERSION
OF NOV GENE IN CHICKEN BERRYONIC FIEROBLASTS (CEF) IS SUFFICIENT
TO INDUCE THE TRANSPORMATION OF CEF IN VITRO.
-1 TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWRR LEVEL IN
MUSCLE AND INTERSTANC, IN THE EMBRYO. LUNG AND LESS SO IN BRAIN AND
SPLEEN, IN ADULT CHICKEN MAY.-INDUCED NEPHROBLASTOMAS EXPRESS A HIGH
ADULT KIDNEY.
ADULT KIDNEY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update).
15-JUN-2002 (Rel. 41, Last annotation update).
NOV protein precursor (Nephroblastoma overexpressed gene protein).
Gallus gallus (Chicken).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crochet J., Perbal B.; "Proviral rearrangements and overexpression of a new cellular gene (nov) in myeloblastosis-associated virus type 1-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Brown leghorn;
MEDLINE=92107157; PubMed=1309586;
Joliot V., Martinerie C., Dambrine G., Plassiart G., Brisac M.,
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   Score 48; DB 1; Length 711;
Pred. No. 0.62;
                                                                        1; Indels
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                                                                    3; Mismatches
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InterPro; IPR000359; Cys knot.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR001084; TSPI.
InterPro; IPR001007; VWF_C.
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Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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Pfam; PF00090; tsp_1; 1.
Pfam; PF00093; vwc; 1.
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SWART; SW00121; IB; 1.
SWART; SW00219; TSP1.
SWART; SW00214; VWC; 1.
PROSITE; PS00222; IGF_B;
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                                                                                                                                     1 CFQLKKNMKKVR 12
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P28686;
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SEQUENCE FROM N.A.

SUZUKI, K., Taklashi M., Imamura S., Ishikawa T.;

Suzuki, K., Taklashi M., Imamura S., Ishikawa T.;

Submitted (XXX-1992) to the EWBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: Urea + H(2/2) + 2 NH(3).

-!- CAFACTOR: Binds 2 nickel ions per submuit (By similarity).

-!- FUM: Lys-222 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).

-!- PUM: Lys-222 is carbamylated. The carbamoyl group provides the similarity: BELONGS TO THE UREASE PAMILY.
                                                                                                                                                                                                                                                                                                                                                             .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Acid urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (BY SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 1; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactobacillus fermentum.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus;
NCBI_TaxID=1613;
                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (PC
1ECB3FA3058C6797 CRC64;
                                                                             binding; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.5;
1; Mismatches
                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                  NOV PROTEIN. VWFC.
                                                                                                          POTENTIAL
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                 PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFC; 1.
Proto-oncogene; Growth factor
                                                                                                                                                                                                                                                                                                                                                                                        38268 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          65.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interPro; IPR001924; UreaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD002467; UreaseA; I
PROSITE; PS00145; UREASE 2;
PROSITE; PS01120; UREASE 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D10605; BAA01460.1; -.
HSSP; P41020; 1UBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00449; urease; 1
Pfam; PF02802; urease_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 CIOTKKSMKAVR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOLKKNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                     351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; M38.UNW;
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                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1078; AMINACHANNEL.
TIGREPMS; TIGROD67; deg-1; 1.
PROSITE; PSO1206; ASC; del.
Hypothetical protein; Ionic channel; Transmembrane; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Magdi L., Gattung S., Bartko L.;
Submitted (AFF-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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                                                                                  Score 42, DB 1; Length 573;
Pred. No. 5.5;
1; Mismatches 3; Indels
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POTENTIAL.
POTENTIAL.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTEN N-LINKED
                                                                                                                      3; Indels
NICKEL 2 (BY SIMILARITY).
BY SIMILARITY
                              Y SIMILARITY.
2D2619781C39E54B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90776 MW; 2CAACF7D41770B54 CRC64;
                                                                                                                                                                                                                                                                                                                  15-JTL-1998 (Rel. 36, Created)
15-JTL-1998 (Rel. 36, Last sequence update)
15-JTN-2002 (Rel. 41, Last annotation update)
Degenerin-like protein ZK770.1 in chromosome
                                                                                                                                                                                                                                                                                   795 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormPep, ZK770.1; CE15411.
InterPro, IPR004726; Deg-1.
InterPro, IPR001873; Na+channel_ASC.
Ffam; PF00858; ASC; 1.
             365 NI
325 BY
61805 MW;
                                                                                  65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U97404; AAB93309.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.6%;
ilarity 70.0%;
Conservative
                                                                                                   Local Similarity 66.7
les 8; Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        ZK770.1.
Caenorhabditis elegans.
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             365
325
373 AA;
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388
458
499
518
795 AA;
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Best Local Similarity
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CARBOHYD
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SEQUENCE
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                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                  001635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ010930; CAA09407.1; -
PDB; 1B1X; 02-DEC-98
PDB; 1B1X; 02-DEC-98
PDB; 1B7Z; 02-FEB-99
PDB; 1B7Z; 02-FEB-99
PDB; 1B7Z; 02-FEB-99
InterPro; IPR001156; Transferrin.
Pfam; PF00455; transferrin; 2.
PRINTS; PR00427; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS002007; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 1.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P. "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Paramasivam M.P., Singh T.P.; Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.; "cDMs sequence of mare lactoferrin."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF AN ANION, USUALLY BICARBONATE.
1- SUBUNIT: MONOMER.
1- SUBCELLULAR LOCATION: Secreted.
1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LACTOTRANSFERRIN
      695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
      STANDARD;
                                                                                                                                                                                                              Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204
1179
1189
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1187
1281
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653
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NON TER 1
SIGNAL <1
TRFL HORSE 077811;
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1; Indels

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329 CFQIKGNVKK 338

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Matches

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Nature 415:871-880(2002)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.1%; Score 41; DB 1; Length 695; 58.3%; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (PC
N-LINKED (GLCNAC. . .) (PC
07BB84D50E1B165D CRC64;
                                                                                                                                                     IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
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Whyszyota; Fungi, Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Hypothetical protein CS82.09 in chromosome II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75991 MW;
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les 7; Conservative
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                                                                                                                                                       66
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                                                                                                                                                                                                                                                                                                                                     METAL
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryōta; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
Cyanidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vogel H., Fischer S., Valentin K. U., "A model for the evolution of the plastid sec apparatus inferred from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Wol. Evol. 51:382-390 (2000).
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. PROBABLY INTERACTS WITH OTHER PROTEINS TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE CHLOROPLAST ENDOPLASMIC RETICCLUM (CER) MEMBRANES.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast.
-!- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gloeckner G., Rosenthal A., Valentin K.-U.; "The structure and gene repertoire of an ancient red algal plastid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 40; DB 1; Length 238; 41.7%; Pred. No. 5.5; 1; Indels ive 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                       EMBL, AL096788, CAB46672.1, -.
Hypothetical protein.
SEQUENCE 238 AA, 26479 MW, 58095AA8CD708180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECY_CYACA STANDARD; PRT; 410 AA. P46249; QSMD55; 10-NOV-1995 (Rel. 32, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preprotein translocase secY subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00303; SECYTRNLCASE.
TIGREAMS; TIGR00967; 3a05018007; 1.
PROSITE; PS00755; SECY 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=RK-1;
MEDLINE=20496959; PubMed=11040290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secY gene phylogeny.";
Plant Mol. Biol. 32:685-692(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97134960; PubMed=8980520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF022186; AAF12924.1; -.
InterPro; IPR002208; SecY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 CYELQQNSKKIK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQLKKNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyanidium caldarium.
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us-09-743-107b-96.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coturnix coturnix japonica (Japanese quail).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
NOV protein precursor (Nephroblastoma overexpressed gene protein)
                                                                                                                                                             ô
PROSITE; PS00756; SECY 2; 1.
Protein transport; Transmembrane; Chloroplast; Translocation. CONFLICT 149 149 MISSING (IN REF. 1).
SEQUENCE 410 AA; 46242 MW; 7CB0130175B1DF03 CRC64;
                                                                                                            Score 39, DB 1; Length 410;
Pred. No. 13;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Growth factor binding; Signal.
1 26 NOV PROTEIN.
172 NWFC.
10 334 CTCK.
10 297 BY SIMILARITY.
131 BY SIMILARITY.
14 329 BY SIMILARITY.
11 329 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                        353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U13063; AAA21128.1; -.
InterPro; IRR00359; Cys knot.
InterPro; IRR000867; Intl_gro_fac_pr.
InterPro; IRR0010067; TSP1.
InterPro; IRR001007; VWF_C.
Fam; PR00007; Cys knot; 1.
Pfam; PR00009; tsp_1; 1.
Pfam; PR00099; tsp_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SM0121; IB; 1.

R SWART; SM00209; TSP1; 1.

R SWART; SM00209; TSP1; 1.

R PROSITE; PS00222; IGF EINDING; 1.

PROSITE; PS01128; CTCK 1; 1.

PROSITE; PS01208; VWPC; 1.

PROSITE; PS01208; VWPC; 1.
                                                                                                               60.9%;
                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                           313 CFELSNNLKK 322
                                                                                                                                 Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                1 CFQLKKNWKK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                 NOV COTJA
P42642;
                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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REFAINISE SUCRACE AND A. MOSZET I., Albertini A.M., Alloni G., REDINE-98044033; PubMed-9384377; Albertini A.M., Alloni G., ALBERTINE-98044033; PubMed-9384377; Albertini A.M., Borchert S., Azevedo V., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Borvilse R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Borvilse R., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Ratian K.D., Errington J., Fabret C., Ferrari E., Foulger D., And Choi S.K., Colaser P., Goffeau A., Golightly B.J., Grandi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Aniseppi G., Guy B.J., Haged K., Halech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Ooris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobaysahi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Modis B., Karamata A., Lardinois S., Lauber J., Lazarevic V., Lardinos A., Lardinois S., Lauber J., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parsecont B., Purnelle B., Rapoport G., Rey M., Reynolds S., Resean E., Polic P., Purnelle B., Rapoport G., Ros M., Tacconi B., Takagi T., Takahashi H., Takemaru K., Sach C., Serio P., Shin B.S., Soldo B., Sorotin M., Taconoi B., Takagi T., Takahashi H., Takemaru K., Andeler E., Walbuter E.,
    296 333 BY SIMILARITY.
276 276 N-LINKED (GLCNAC. . .) (POTENTIAL.)
353 AA, 38667 MW, 717D9F8S33882E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kooistra J., Venema G.;
"Cloning, sequencing, and expression of Bacillus subtilis genes
involved in ATP-dependent nuclease synthesis.";
J. Bacteriol. 173:3644-3655(1991).
                                                                                                                                                                                                                                                       ö
                                                                                                                                                             Score 38, DB 1; Length 353;
Pred. No. 17;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STFAIN=168;
Noback M.A., Terpstra P., Holsappel S., Venema G., Bron
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
ATP-dependent nuclease subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=0G1;
MEDLINE=91267926; Pubmed=1646786;
                                                                                                                                                         Query Match 59.4%;
Best Local Similarity 58.3%;
Matches 7; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                      260 CIRTKKSMKAVR 271
                                                                                                                                                                                                                                                                                                                       1 CFQLKKNMKKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmic
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDB BACSU
DISULFID
CARBOHYD
SEQUENCE
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ADDB_BACSU
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Best Loca
Matches
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Y504_BORBU
       STKB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A39432; A39432.
Subtilist; BG10465; addB.
LinterPro; IPR000512; Uvrb-helicase.
Pfam; PF00580; Uvrb-helicase; 1.
Hydrolase; Nuclease; Exonuclase; Endonuclease; Helicase; ATP-binding; DNA repair; Complete proteome.

NP BIND 1 22 ATP (POTENTIAL).
FUNCTION: THE ENZYME COMPLEX MAY HAVE A WIDE VARIETY OF CATALYTIC ACTIVITIES INCLUDING ATP-DEPENDENT EXONUCLEASE, ATP-STIMULATED ENDONUCLEASE, ATP-DEPENDENT HELICASE AND DNA-DEPENDENT ATPASE
                                                                SUBUNIT: THE B.SUBTILIS ATP-DEPENDENT NUCLEASE COMPLEX IS FORMED BY ONE B SUBUNIT IN CONJUNCTION WITH ONE A SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
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                                                                                                                                                                                                                                                                                                                                                                                                            NP BIND 1 22 ATP (POTENTIAL).
SEQUENCE 1166 AA; 134631 MW; 1A57BBE81A08AB4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypothetical protein (Fragment).
Mycoplasma capricolum.
Bacteria, Firmicutes; Mollicutes; Entomoplasmatales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001454; Hlgnase/hydrlase.
InterPro; IPR000150; Hypothet_cof.
                                                                                                                                                                                                                                                     EMBL; M63489; AAA22200.1; -.
EMBL; Y14081; CAA74481.1; -.
EMBL; Z99109; CAB12902.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000150; Hypothet
Pfam; PF00702; Hydrolase; 1
PROSITE; PS01228; COF_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z33006; CAA83689.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Owery Match
Best Local Similarity 63.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 FOLOKRMKKAK 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FOLKKNIMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Entomoplasmataceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2095;
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125_MYCCA
D _Y125_MYCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATC 35210 / B31;
STRAIN=ATC 35210 / B31;
MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey B.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Paliner N., Adams M.D., Gocayne J.D., Wetdman J.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.,
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; Pruzso, ..., SMART; SMO471; HD; 1.

TIGREAMS; TIGR00277; HDIG; 1.

PROSITE; PS50084; KH TYPE 1; 1.

PROSITE; PS50084; KH TYPE 1; 1.

Hypothetical protein; Transmembrane; RNA-binding; Complete proteome. TRANSMEM 2 2 KH.
                                                                                                                                                                                                      .
0
                                                                                                                                        57.8%; Score 37; DB 1; Length 267; 50.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 510; 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                   2; Indels
PROSITE; PS01229; COF_2; 1.
Hypochetical protein.
NON TER
SEQÜENCE 267 AA; 30425 MW; DS912DD5B39A8451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58002 MW; A85D675FEA63C668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:580-586(1997).
-- SIMILARITY: BELOWGS TO THE UPF0144 FAMILY.
-- SIMILARITY: CONTAINS 1 HD DOMAIN.
-- SIMILARITY: CONTAINS 1 KH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein BB0504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 AA.
                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002819; HD.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH type 1.
InterPro; IPR003607; ME type 1.
Ffam; PF00013; KH-domain; 1.
Pfam; PF001966; HD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001153; AAC66875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.8%;
                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                      1 CFQLKKNMKKVR 12
                                                                                                                                                               Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Y504 BORBU
O51457;
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      Gaps
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Oguri T., Katoh O., Takahashi T., Isobe T., Kuramoto K., Hirata S.,
Manakido M., Matanabe H.;
"The kruppel-type zinc finger family gene, HKRI, is induced in lung
cancer by expecter to platinum drugs.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 314-537 FROM N.A.

MEDLINE=89068696; PubMed=2850480;

Ruppel J. M., Kinzler K.W., Wong A.J., Bigner S.H., Kao F.T.,

Law M.L., Seuancz H.N., O'Brien S.J., Vogelstein B.;

The Gil-Kruppel family of human genes.";

Mol. Cell. Biol. 8:3104-3113 (1988)

-!- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.

-!- SUBCELIVILAR LOCATION: Nuclear (Potential).

-!- SIMILARITY: BELONGS TO THE KRUBPPEL FAMILY OF CZHZ-TYPE ZINC-

FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SW00349; KRAB; 1.
SWART; SW0035; ZAF C2H2; 13.
PROSITE; PSS00805; KFAB; 1.
PROSITE; PSS00028; ZAM FINGER C2H2 1; 13.
PROSITE; PSS0157; ZINC_FINGER C2H2 2; 13.
TRANSCRIPT; PROSITE; PSS0157; ZINC_FINGER C2H2 2; 13.
                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                               HKRI HUMAN STANDARD; PRT; 697 AA.
P10072; Q9UM09;
01-MAR-1989 (Rel. 10, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Krueppel-related zinc finger protein 1 (HKR1 protein) (Fragment).
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     Indels
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   Mismatches
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C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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EMBL; M20675; -; NOT_ANNOTATED_CDS.
PTR; C31201; C31201.
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InterPro; IPR000822; Znf C2H2.
Pfam; PF00096; zf-C2H2; Ī3.
Pfam; PF01352; KRAB; 1.
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jenew; HGNC:4928; HKR1.
                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                4 LKKNMKKVR 12
                                                   LEKNLKKVR 39
7 ;
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ZN_FING
ZN_FING
ZN_FING
                                                                                                                RESULT 12
HKR1_HUMAN
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Mammary gland;
Paramasivam M., Stingh R., Sahani M.S., Singh T.P.;
Paramasivam M., Stiniusean A., Singh R., Sahani M.S., Singh T.P.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ARONS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
-!- SUBGILLIAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEGUENCE FROM N.A.
STRAIN-Somali; TISSUE-Lactating mammary gland;
Kappellar S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                      Score 37; DB 1; Length 697;
Pred. No. 48;
1; Mismatches 3; Indels
C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
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LACTOTRANSFERRIN
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Pfam; PF00405; transferrin; 2.
PRINTS; PR00425; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 2; 2.
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                                                                                                                                                                                                 79552 MW;
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667
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673
697 AA;
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Best Local Similarity
Matches 6; Conserv
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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(POTENTIAL).
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TISSUB-Endothelial cells;

MEDLINE=95353875; PubMed=7627717;

MEDLINE=95353875; PubMed=7627717;

MEDLINE=95353875; PubMed=7627717;

Golay J., Introna M., Gulino D., Lampugnani M.G., Dejana E.;

"Functional properties of human vaceular endothelial cadherin (7B4/Cadherin-5), an endothelium-ppecific cadherin.";

Arterioscler. Thromb. Vasc. Biol. 15:1229-1239(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.8%; Score 37; DB 1; Length 708; 58.3%; Pred. No. 49; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
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G -> A (IN REF. 2).
S -> P (IN REF. 2).
LLS -> PLF (IN REF. 2).
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2. SIMILARITY.
BY SIMILARITY.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQLKKNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 CAQWQRRMKKVR 49
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708 AA;
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PRESIDENCE FROM N.A.

MINIOLINES AND CATES. PROCHEME S. MAILER N.A.;

MINIOLINES AND CATES. PRACEMES P. MAILER N. MARCHING AND CATES. PRACEMES PROCESSARIAN OF PROCESSARIAN OF PARTIAL STATES. PRACEMENTS. PROCESSARIAN OF PARTIAL STATES. PROCESSARIAN OF PARTIAL STATES. PRACEMENTS. PRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M. Chung E., Duncan M., Guznan E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Hyman R., Roberts A., Nomath A., Norgeren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl B., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Smith V., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ datebases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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01-FEB-1995 (Rel. 31, Last Sequence update)
01-FEB-1995 (Rel. 31, Last amotation update)
Hypothetical 31.4 kDa protein in GCN4-WBP1 intergenic region.
                                                    VASCULAR ENDOTHELIAL-CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 784;
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                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Hypothetical protein.
SEQUENCE 282 AA; 31364 MW; 8F7CA122F91E491A CRC64;
                                                                          EXTRACELLULAR (POTENTIAL
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Best Local Similarity 77.8%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches
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784 AA;
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Db 86 QLKKSLKKV 94
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Search completed: February 21, 2003, 07:51:44 Job time : 7.2093 secs

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08tcd2 homo sapien
09sf6 lactobacill
020s62 caenorhabdi
09ucy5 homo sapien
091z65 arabidopsis
09723 clostridium
09bdy9 homo sapien
09bl17 homo sapien
09hl16 aenorhabdi
07385 plasmodium
094e36 oryza sativ
022774 caenorhabdi
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                   M protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Q986F6
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Q9TG3
Q9HQX9
Q9HQX9
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Q9SG111
Q94E36
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_bacteria:*
sp_fungi:*
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                                                                                                                                                        1 CPQLKKNWKKVR 12
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erfect score:
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		24 37	57.8	546	16	Q98PL7	Q98pl7 mycoplasma
			57.8	565	16	Q8XJU2	N
			57.8	718	Ŋ	Q23447	Q23447 caenorhabdi
			57.8	720	ø	C0N6O	
			56.2	81	16	Q97PW0	
-			56.2		16	Q97TB1	
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			56.2		Ŋ	095248	Q95248 plasmodium
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			56.2		0	Q9X319	
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	8	Q8TCD2		PRELIMINARY;		PRT; 711 AA.	
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	3 E	01-100		Tremblrel.	27,	Created) Test semionic undate)	
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-	DE	Lactotransferrin.	G				
	So	Homo sapiens (Human)	mH) Su				
	ပ္ပင္	Eukaryota; Metazoa;	Metazo		data		щ
	38	NCBI TaxID=9606;	sucher: :9606;		Frimaces;	; catarrill; Hominidae;	HOMO.
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	КР	SEQUENCE FROM N.A	ROM N.2	ن			

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Gaps
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                                                                                                67.2%; Score 43; DB 4; Length 711; 63.6%; Pred. No. 27; ative 3; Mismatches 1; Indels
SEQUENCE FROM N.A.
TISSUE=PROSTATE;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022347; AAH22347.1; -
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNM-2002 (TrEMBLrel. 21, Last annotation update)
Urease (EC 3.5.1.5) (Urea amidohydrolase).
Lactobacillus fermentum.
                                                                                                                                                                                                                                                                  573 AA
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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198 CFLIRKNWKRVK 209
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21 FQWQRNMRKVR 31
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HSSP; P02788; 1BKA.
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Q9LZ65
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Q9UCY5
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Rhabditidae, Peloderinae, Caenorhabditis.
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Bacteria, Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Lactobacillaceae; Lactobacillus.
NCBI_TaxID=1613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.6%; Score 42; DB 2; Length 573; 66.7%; Pred. No. 34; arive 1; Mismatches 3; Indels
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Geisel C., Bradahaw H.;
"The sequence of C. elegans cosmid F48D6.";
submitted (WAX-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
"Direct Submission.";
"Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U58732; AAB00596.1; -.
Hypothetical protein.
SEQUENCE 333 AA; 38150 MW; B2A5ED557CDBA5C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 38.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 A.A.
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MEDLINE=99069613; PubMed=9851916;
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Best Local Similarity 66./-
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1 CFQLKKNMKKVR 12

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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Rna binding protein-like (AT5g04600/T32M21_200) (Putative RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T32M212200 OR AT5G04600.
Azabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,

Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka

Nayvan M., Onodera C.S., Palm R.J., Pham P.K., Quach H.L., Sakurai

Sacou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.
Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.9%; Score 39; DB 4; Length 38; 63.6%; Pred. No. 11; 1. Indels ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001115; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
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MEDLINE=96081613; PubMed=8551695;
Sato I.;
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Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M., Cavaler-Smith T., Maier U., Douglas S.; "Chloroplast protein and centrosomal genes, a tRNA intron, and odd telomeres in an unusually compact eukaryotic genome, the cryptomonad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=21223349; PubMed=11323671;

Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng Wu X., Reith M., Cavalier-Smith T., Maier U.;

"The highly reduced genome of an enslaved algal nucleus.";

Nature 410:1091-1096(2001).

EMBL; AJ010592; CAC27001.1; -.
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80.0%; Pred. No. 70;
.ive 0; Mismatches 2; Indels
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL096677; CAC34610.1;
HSSP; Q05516; 1CS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 339 AA; 41403 MW; B24EE99E30715629 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DJ322G13.2.2 (Zinc finger protein FLJ21794, isoform 2)
DJ322G13.2.
                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLEE1. 17, Created)
01-JUN-2001 (TrEMBLEE1. 17, Last sequence update)
01-DEC-2001 (TrEMBLEE1. 19, Last annotation update)
Hypothetical 41.4 kDa protein.
6011lardia theta (Cryptomonas phi).
Eukaryota Cryptophyta; Cryptomonadaceae; Guillardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 97:200-205(2000)
                                              Mismatches
                     Pred. No.
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MEDLINE=20087226; Pubmed=10618395;
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InterPro; IPR000822; Znf_C2H2.
Pfam; PP000651; BTB; 1.
Pfam; PP000065; Zf_C2H2; 5.
SMART; SM0025; BTB; 1.
SMART; SM00355; ZnF_C2H2; 5.
                58.3%;
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Best Local Similarity 90.0،
المراقعة Si Conservative
                Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleomorph.";
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Q9AW69
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Yamada K., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H.,

Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Kim C., Koesema B., Lam B., Lin J., Mayers M.C., Miranda M.,

Narusaka M., Nguyen M., Sakurai T., Satou M., Seki M.,

Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

"Full Length cDNA of gene At5g04600 (G1:15238220).",

Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

"Full Length cDNA of gene At5g04600 (G1:15238220).",

EMBL, A152895; CAB85566.1;

EMBL, A278899; AAK56701;

EMBL, A278899; AAK56702.1;

EMBL, A278899; AAK56702.1;

EMBL, A2878899; AAK56702.1;

EMBL, A2878899; Exm, 1.

SWART; SM00360; RRM, 1.

PROSITE; PSS0102; RRM, 1.

PROSITE; PSS0102; RRM, 1.

SRQUENCE 222 AA; 25262 MW; BA47EAEGDBB2F153 CRC64;
                                                                                                  Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.
Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T.,
Satcu M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
"Arabidopsis cDNA clones."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 824 / DSM 792 / VKW B-1787,
MEDLINE=21359325; PubMed=11466286;
Noelling J., Ereton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Glbson R., Lee H.M., Dubols J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smitt D.R.,
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.",
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Bacteria, Firmicutes, Bacillus/Clostridium group, Clostridia,
Clostridiales, Clostridiaceae, Clostridium.
NCBI_TaxID=1488;
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"Arabidopsis ORF clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                 Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Uncharacterized conserved protein.
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J. Bacteriol. 183:4823-4838(2001).
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Complete proteome.
SEQUENCE 282 AA; 31629 MW
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Best Local Similarity 100.(
Matches 8; Conservative
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SEQUENCE FROM N.A.
                                                                            SEQUENCE FROM N.A.
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Gaps

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Caenorhabditis elegans.
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ID 07
AC 07
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01-MAR-2001 (TERMELRE1. 16, Created)
01-MAR-2001 (TERMELRE1. 16, Last sequence update)
01-UNA-2002 (TERMELRE1. 12, Last annotation update)
01-JUN-2002 (TERMELRE1. 21, Last annotation update)
DJ322G13.2.3 (zinc finger protein FLJ21794, isoform 3).
Homo sapiens (Human)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
REMBL, AL096677; CAC17422.1;
RISSP: PO7248; 1ARR.
RICEZPRO; IPRO00210; BTB POZ.
RICEZPRO; IPRO00822; Znf_C2H2.
R Pfam; PP000651; BTB, 1.
R Pfam; PP000063; Znf_C2H2.
R Probom; PD000003; Znf_C2H2; B.
R SWART; SW00255; BTB; 1.
R SWART; SW00255; BTB; 1.
R SWART; SW00355; Znf_C2H2; 8.
                                                                                                                                           60.9%; Score 39; DB 4; Length 455; 87.5%; Pred. No. 90; Live 0; Mismatches 1; Indels
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
PROSITE; PS50097; BTB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS501S7; ZINC_FINGER_C2H2_2; 5.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 455 AA; 51357 WW; 33089B1B7F7CB757 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ322G13.2.1 (zinc finger protein FLJ21794, isoform 1)
DJ322G13.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWANT; SNUOJS); ALLE_LELE; O.
PROSITE; PS50097; BTE; 1.
PROSITE; PS00189; ZINC FINGER_C2H2_1; 7.
PROSITE; PS501197; ZINC_FINGER_C2H2_2; 8.
DNA-Dinding; Metal binding; Zinc-finger.
SEQUENCE 545 AA; 61982 MW; AAA98203319C361E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            545 AA
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                                                                                                                                      Query Match 60.9
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             125 CFQLKKQM 132
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9H116
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1043 CFQL-KNMKQI 1052

01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-UUN-2002 (TrEMBLrel. 21, Last annotation update)

CDC2-related protein kinase. PFC0755C, MAL3P6.10.

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SEQUENCE FROM N.A.

MEDLINE=20087226; PubMed=10618395;
Zauner S., Faunholz M., Wastl J., Penny S.L., Beaton M.,
Zauner S., Faunholz M., Waler U., Douglas S.;
"Chloroplast protein and centrosomal genes, a tRNA intron, and odd
telomeres in an unusually compact eukaryotic genome, the cryptomonad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kershaw J.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
|- «TWILLARITY: WEAK, TO C.ELEGANS ZK1193.2 AND TO THE C-TERMINAL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L., W. X., Relth M., Cavaller-Smith T., Maier U.;
"The highly reduced genome of an enslaved algal nucleus.";
Nature 410:1091-1096(2001).
Rhypcheltal AJ010592; CAC27085.1; -.
Hypothetical protein.
SEQUENCE 325 AA; 39399 MW; 27D35E07CD82F083 CRC64;
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Ol-Jun-2001 (TrEMBLrel. 17, Created)
Ol-Jun-2001 (TrEMBLrel. 17, Last sequence update)
Ol-DuN-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 39.4 kDa protein.
Hypothetical 19.4 kDa protein.
Eukaryota, Cryptomonas phi).
Eukaryota, Cryptomonas phi).
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MEDLINE=21223349; PubMed=11323671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAB07849.1; JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleomorph.";
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Q22774
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Probon; PD000001; Euk pkinase; 2.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
ISS3 AA; 182218 MW; E23D3C3416F1E8EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
05UNBD0032H19-19 protein.
07Yza sativa (Rice).
07Yza sativa (Rice).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Entartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
07Yza sativa (Office).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  falciparum .";

Nuture 400:532-538(1999).

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; Z98551; CAB11141.1; --

InterPro; IPR00219; Buk pkinase.

InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sabaki T., Matsumoto T., Yamamoto K.;
Gryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:OSJNBb0032H19.";
Plasmodium Falciparum (isolate 3D7).
Bukaryota, Alveolata; Apicomplexa, Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.9%; Score 39; DB 5; Length 1553; 77.8%; Pred. No. 2.5e+02; 1ve 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone:OSUNBb0032Hi9.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003219; BAB61186.1;
InterPro; IRR03653; SUMO protease.
Pfam; PF02902; Peptidase C48; 1.
SEQUENCE 1167 AA; 131408 MW; 6308AB28A292C1F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.2%; Score 38.5; DB 10; 72.7%; Pred. No. 2.46+02; ive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1167 AA
                                                                                                                                                                                                             MEDLINE=99376085; PubMed=10448855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 77,8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duery Match
Sest Local Similarity 72.7
Aatches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQLKKNMKKV 11
                                                                                                                                                  SEQUENCE FROM N.A.
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Query Match

SULT 13 4E36

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Gaps

; 0

Indels

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R InterPro; IPR001304; Lectin_C.
R InterPro; IPR002035; VWF_A.
P fam, PP000059; Lectin_c; 1.
R SMART; SW00181; EGF; 3.
R SMART; SW00181; EGF; 3.
R SMART; SW00181; EGF; 3.
R PROSITE; PS00022; EGF 1; UNKNOWN S.
R PROSITE; PS01186; EGF 2; 3.
R PROSITE; PS01284; VWFĀ; 1.
R PROSITE; PS00284; VWFĀ; 1.
W Hypothetical protein.
W Hypothetical protein.
O SEQUENCE 2014 AA; 221261 WW; 65E3BG76440C73BB CRC64;
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Query Match 59.4%; Score 38; DB 5; Length 2014; Best Local Similarity 87.5%; Pred. No. 4.7e+02; Matches 7; Conservative 1; Mismatches 0; Indels 

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earch completed: February 21, 2003, 08:00:50 ob time : 23.6744 secs